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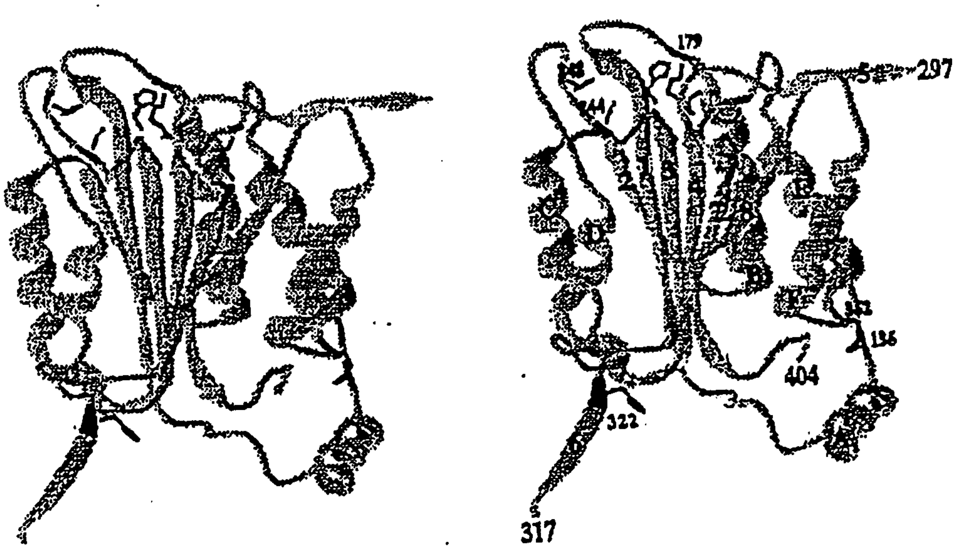

(57) Abstract

Interleukin-1β converting enzyme ("ICE") processes an inactive precursor to the pro-inflammatory cytokine, interleukin-1β. The high-resolution structure of human ICE crystallized in complex with an inhibitor is determined by X-ray diffraction. The active site spans both the 10 and 20 kilodalton subunits. The accessory binding site is composed of residues from the p10 and p20 subunits that are adjacent to the two-fold axis of the crystal. The structure coordinates of the enzyme may be used to design novel classes of ICE inhibitors.

CRYSTAL STRUCTURE AND MUTANTS OF INTERLEUKIN-1ß CONVERTING ENZYME

TECHNICAL FIELD OF INVENTION

The present invention relates to crystals of interleukin-1ß converting enzyme ("ICE") and more particularly to the high resolution structure of ICE obtained by X-ray diffraction. This invention also relates to mutants of ICE. In addition, this invention relates to methods of using the structure coordinates of ICE and mutants thereof to screen and design compounds that bind to the active site and accessory binding site of ICE.

BACKGROUND ART

Interleukin-1 ("IL-1") is a major pro-inflammatory and immunoregulatory protein that stimulates fibroblast differentiation and proliferation, the production of prostaglandins, collagenase and phospholipase by synovial cells and chondrocytes, basophil and eosinophil degranulation and neutrophil activation. Oppenheim, J.H. et al, Immunology Today, 7, pp. 45-56 (1986). As such, it is involved in the pathogenesis of chronic and acute inflammatory and autoimmune diseases. IL-1 is predominantly produced by peripheral blood monocytes and exists in two distinct agonist forms, IL-1α and IL-1ß. Mosely, B.S. et al., Proc. Nat. Acad. Sci., 84,

pp. 4572-4576 (1987); Lonnemann G. et al., Eur.J. Immunol., 19, pp. 1531-1536 (1989).

IL-1ß is synthesized as a biologically inactive precursor, pIL-1ß. pIL-1ß is a 33kDa polypeptide that lacks a conventional leader sequence and is not processed by a signal peptidase. March, C.J., Nature, 315, pp. 641-647 (1985). Instead, pIL-1ß is cleaved by interleukin-1ß converting enzyme ("ICE") between Asp 116 and Ala 117 to produce the biologically active C-terminal fragment of 17kDa molecular weight found in serum and synovial fluid. Sleath, P.R. et al., J. Biol. Chem., 265, pp. 14526-14528 (1992); Howard, A.D. et al., J. Immunol., 147, pp. 2964-2969 (1991). Processing by ICE is also necessary for the transport of mature IL-1ß through the cell membrane.

ICE is a cysteine protease localized primarily in monocytes. It converts precursor IL-1ß to the mature form. Black, R.A. et al., FEBS Lett., 247, pp. 386-390 (1989); Kostura, M.J. et al., Proc. Natl. Acad. Sci. USA, 86, pp. 5227-5231 (1989). ICE, or its homologues, also appears to be involved in the regulation of cell death or apoptosis. Yuan, J. et al., Cell, 75, pp. 641-652 (1993); Miura, M. et al., Cell, 75, pp. 653-660 (1993); Nett-Fiordalisi, M.A. et al., J. Cell Biochem., 17B, p. 117 (1993). In particular, ICE or ICE homologues are thought to be associated with the regulation of apoptosis in neurogenerative diseases, such as Alzheimer's and Parkinson's disease. Marx, J. and M. Baringa, Science, 259, pp. 760-762 (1993); Gagliardini, V. et al., Science, 263, pp. 826-828 (1994).

ICE has been previously described as a heterodimer composed of two subunits, p20 and p10 (20kDa and 10kDa molecular weight, respectively). These subunits are derived from a 45kDa proenzyme (p45)

by way of a p30 form, through an activation mechanism that is autocatalytic. Thornberry, N.A. et al., Nature, 356, pp. 768-774 (1992). The ICE proenzyme has been divided into several functional domains: a prodomain (p14), a p22/20 subunit, a polypeptide linker and a p10 subunit. Thornberry et al., supra; Casano et al., Genomics, 20, pp. 474-481 (1994).

Full length p45 has been characterized by its cDNA and amino acid sequences. PCT patent applications WO 91/15577 and WO 94/00154. The p20 and p10 cDNA and amino acid sequences are also known. Thornberry et al., supra. Murine and rat ICE have also been sequenced and cloned. They have high amino acid and nucleic acid sequence homology to human ICE. Miller, D.K. et al., Ann. N.Y. Acad. Sci., 696, pp. 133-148 (1993); Molineaux, S.M. et al., Proc. Nat. Acad. Sci., 90, pp. 1809-1813 (1993). Knowledge of the primary structure of ICE, however, does not allow prediction of its tertiary structure. Nor does it afford an understanding of the structural, conformational and chemical interactions of ICE and its substrate pIL-1ß or other substrates or inhibitors.

ICE inhibitors represent a class of compounds useful for the control of inflammation or apoptosis or both. Peptide and peptidyl inhibitors of ICE have been described. PCT patent applications WO 91/15577; WO 93/05071; WO 93/09135; WO 93/14777 and WO 93/16710; and European patent application 0 547 699. However, due to their peptidic nature, such inhibitors are typically characterized by undesirable pharmacologic properties, such as poor oral absorption, poor stability and rapid metabolism. Plattner, J.J. and D.W. Norbeck, in Drug Discovery Technologies, C.R. Clark and W.H. Moos, Eds. (Ellis Horwood, Chichester, England, 1990), pp. 92-

126. This has hampered their development into effective drugs.

SUMMARY OF THE INVENTION

The present invention solves the above problems.

It is an object of this invention to solve the three-dimensional structure of interleukin-1ß converting enzyme ("ICE") and to determine its structure coordinates.

It is an object of this invention to use the structure coordinates of an ICE crystal to reveal the atomic details of the active site and one or more accessory binding sites of the enzyme.

It is also an object of this invention to use the structure coordinates of an ICE crystal to solve the structure of a different ICE crystal, or a crystal of a mutant, homologue or co-complex, of ICE.

It is a further object of this invention to provide interleukin-1ß converting enzyme mutants characterized by one or more different properties as compared with wild-type ICE. These properties include altered surface charge, increased stability to subunit dissociation, altered substrate specificity or higher specific activity. ICE mutants are useful to identify those amino acids that are most important for the enzymatic activity of ICE. This information, in turn, allows the design of improved inhibitors of ICE as compared with peptidic ICE inhibitors.

It is also an object of this invention to use the structure coordinates and atomic details of ICE, or its mutants or homologues or co-complexes, to design, evaluate computationally, synthesize and use inhibitors of ICE that avoid the undesirable physical and pharmacologic properties of peptidic ICE inhibitors.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 represents a ribbon drawing of the p20/p10 interleukin-1ß converting enzyme heterodimer. The active site is at the top of the figure, roughly at the center of the cluster of displayed side chains.

Figure 2 represents a space-filling model of the $(p20)_2/(p10)_2$ tetramer of interleukin-1ß converting enzyme. Two p20 subunits (dark shade) are in contact with two p10 subunits (light shade). Black shading on top left and bottom right represents a tetrapeptide aldehyde inhibitor bound in each of the two active sites of the tetramer. The crystallographic two-fold axis is approximately perpendicular to the plane of drawing, and runs through the small hole at the center of the interface between the two p10 subunits. The N- and C-terminal ends of each subunit are labeled.

Figure 3 is a graphic depiction of the activity of various interleukin-1ß converting enzyme mutants in processing pIL-1ß intracellularly, relative to wild-type interleukin-1ß converting enzyme activity. The particular mutants tested are designated on the x-axis using nomenclature listing the specific amino acid and its residue number. For example, "C285S" indicates replacement of amino acid Cys-285 with serine. Activity levels were measured at 16 hours (hatched bar) and 24 hours (solid bars).

BRIEF DESCRIPTION OF THE TABLES

Table A lists the amino acids of ICE that constitute the tetramer interface contacts between the ICE subunits and that constitute the accessory binding site moiety.

Table B lists the atomic structure coordinates for ICE as derived by X-ray diffraction

from a crystal of ICE complexed to a tetrapeptide inhibitor.

ABBREVIATIONS AND DEFINITIONS

ABBREVIATIONS

Amino Acids

A = Ala = Alanine
V = Val = Valine
L = Leu = Leucine
I = Ile = Isoleucine
P = Pro = Proline
F = Phe = Phenylalanine
W = Trp = Tryptophan
M = Met = Methionine
G = Gly = Glycine
S = Ser = Serine
T = Thr = Threonine
C = Cys = Cysteine
Y = Tyr = Tyrosine
N = Asn = Asparagine
Q = Gln = Glutamine
D = Asp = Aspartic Acid
E = Glu = Glutamic Acid
K = Lys = Lysine
R = Arg = Arginine
H = His = Histidine

DEFINITIONS

The following terms are also used herein:

The term "naturally occurring amino acids" means the L-isomers of the naturally occurring amino acids. The naturally occurring amino acids are glycine, alanine, valine, leucine, isoleucine, serine, methionine, threonine, phenylalanine, tyrosine, tryptophan, cysteine, proline, histidine, aspartic

acid, asparagine, glutamic acid, glutamine, γ-carboxyglutamic acid, arginine, ornithine and lysine. Unless specifically indicated, all amino acids referred to in this application are in the L-form.

The term "unnatural amino acids" means amino acids that are not naturally found in proteins. Examples of unnatural amino acids used herein, include racemic mixtures of selenocysteine and selenomethionine. In addition, unnatural amino acids include the D or L forms of nor-leucine, para-nitrophenylalanine, homophenylalanine, para-fluorophenylalanine, 3-amino-2-benzylpropionic acid, homoarginine, and D-phenylalanine.

The term "positively charged amino acid" includes any naturally occurring or unnatural amino acid having a positively charged side chain under normal physiological conditions. Examples of positively charged naturally occurring amino acids are arginine, lysine and histidine.

The term "negatively charged amino acid" includes any naturally occurring or unnatural amino acid having a negatively charged side chain under normal physiological conditions. Examples of negatively charged naturally occurring amino acids are aspartic acid and glutamic acid.

The term "hydrophobic amino acid" means any amino acid having an uncharged, nonpolar side chain that is relatively insoluble in water. Examples of naturally occurring hydrophobic amino acids are alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine.

The term "hydrophilic amino acid" means any amino acid having an uncharged, polar side chain that is relatively soluble in water. Examples of naturally occurring hydrophilic amino acids are serine, infra,

threonine, tyrosine, asparagine, glutamine, and cysteine.

The term "mutant" refers to an ICE polypeptide, i.e.. a polypeptide displaying the biological activity of wild-type, human ICE, characterized by the replacement of at least one amino acid from the wild-type, human ICE sequence according to Thornberry, N.A. et al., Nature, 356, pp. 768-774 (1992). Such a mutant may be prepared, for example, by expression of ICE cDNA previously altered in its coding sequence by oligonucleotide-directed mutagenesis.

ICE mutants may also be generated by site-specific incorporation of unnatural amino acids into ICE proteins using the general biosynthetic method of Noren, C.J., et al., Science, 244, pp. 182-188 (1989). In this method, the codon encoding the amino acid of interest in wild-type ICE is replaced by a "blank" nonsense codon, TAG, using oligonucleotide-directed mutagenesis (described in detail, infra). A suppressor tRNA directed against this codon is then chemically aminoacylated in vitro with the desired unnatural amino acid. The aminoacylated tRNA is then added to an in vitro translation system to yield a mutant ICE enzyme with the site-specific incorporated unnatural amino acid.

Selenocysteine or selenomethionine may be incorporated into wild-type or mutant ICE by expression of ICE-encoding cDNAs in auxotrophic E. coli strains. Hendrickson, W.A. et al., EMBO J., 9(5), pp. 1665-1672 (1990). In this method, the wild-type or mutagenized ICE cDNA may be expressed in a host organism on a growth medium depleted of either natural cysteine or methionine (or both) but enriched in selenocysteine or selenomethionine (or both).

The term "altered surface charge" means a change in one or more of the charge units of a mutant polypeptide, at physiological pH, as compared to wild-type ICE. This is preferably achieved by mutation of at least one amino acid of wild-type ICE to an amino acid comprising a side chain with a different charge at physiological pH than the original wild-type side chain.

The change in surface charge is determined by measuring the isoelectric point (pI) of the polypeptide molecule containing the substituted amino acid and comparing it to the isoelectric point of the wild-type ICE molecule.

The term "high specific activity" refers to a specific activity of ICE where the second-order rate constant (k_{cat}/K_m) for hydrolysis of the substrate Ac-Tyr-Val-Ala-Asp-aminomethylcoumarin exceeds 7 x 10^4 $M^{-1}s^{-1}$ at 25°C, using the assay described by Pennington, M.W. and N.A. Thornberry, Peptide Res., 7(2), pp. 72-76 (1994). Alternatively, the specific activity of ICE may be determined by monitoring hydrolysis of the substrate Ac-Tyr-Val-Ala-Asp-p-nitroaniline. Reiter, L.A., Intr. J. Peptide Protein Res., 43, pp. 8796 (1994).

The term "altered substrate specificity" refers to a change in the ability of a mutant ICE to cleave a substrate as compared to wild-type ICE. Substrate specificity may be measured by hydrolysis of fluorogenic peptide substrates or of unmodified peptide substrates by ICE, as described in Thornberry et al., supra. ICE mutants with altered substrate specificity demonstrate a second order rate constant (k_{cat}/K_m) for a substrate X_1-Tyr-Val-Ala-X_2-X_3 that exceeds the k_{cat}/K_m for the analogous peptide substrate, X_1-Tyr-Val-Ala-Asp-X_3. For both substrates, X_1 is an amino protecting

group, such as acetyl; X_2 is a natural or unnatural amino acid residue other than L-aspartate; and X_3 is a carboxyl protecting group, such as aminomethylcoumarin or p-nitroaniline.

The "kinetic form" of ICE refers to the condition of the enzyme in its free or unbound form or bound to a chemical entity at either its active site or accessory binding site.

A "competitive" inhibitor is one that inhibits ICE activity by binding to the same kinetic form, of ICE, as its substrate binds -- thus directly competing with the substrate for the active site of ICE. Competitive inhibition can be reversed completely by increasing the substrate concentration.

An "uncompetitive" inhibitor is one that inhibits ICE by binding to a different kinetic form of the enzyme than does the substrate. Such inhibitors bind to ICE already bound with the substrate and not to the free enzyme. Uncompetitive inhibition cannot be reversed completely by increasing the substrate concentration.

A "non-competitive" inhibitor is one that can bind to either the free or substrate bound form of ICE.

Those of skill in the art may identify inhibitors as competitive, uncompetitive or non-competitive, by computer fitting enzyme kinetic data using standard equations according to Segel, I.H., Enzyme Kinetics, J. Wiley & Sons, (1975). It should also be understood that uncompetitive or non-competitive inhibitors according to this invention may bind to the accessory binding site.

The term "homologue" means a protein having at least 30% amino acid sequence identity with ICE or any functional domain of ICE as defined by Thornberry et al., supra and Casano et al., supra.

The term "subunit dissociation" refers to the fact that at very high dilutions of wild-type ICE, or at concentrations of the enzyme below 10 nM, enzymatic activity shows a time dependent loss assayed in the presence of a tetrapeptide substrate. Reconcentration of the dilute, inactive mixture results in complete recovery of ICE activity. Wild-type ICE demonstrates a Kd for subunit dissociation between 1 and 10 nM. Enzymatic activity is determined by measuring the activity of ICE according to the assay of Pennington and Thornberry, supra, at varying concentrations of the enzyme. The concentration of the enzyme is determined by active site titration.

The term "co-complex" means ICE or a mutant or homologue of ICE in covalent or non-covalent association with a chemical entity or compound.

The term "associating with" refers to a condition of proximity between a chemical entity or compound, or portions thereof, and an ICE molecule or portions thereof. The association may be non-covalent -- wherein the juxtaposition is energetically favored by hydrogen bonding or van der Waals or electrostatic interactions -- or it may be covalent.

The term "ß-sheet" refers to the conformation of a polypeptide chain stretched into an extended zig-zig conformation. Portions of polypeptide chains that run "parallel" all run in the same direction. Polypeptide chains that are "antiparallel" run in the opposite direction from the parallel chains.

The term "active site" or "active site moiety" refers to any or all of the following sites in ICE: the substrate binding site; the site where the tetrapeptide inhibitor binds and the site where the cleavage of a substrate occurs. The active site is characterized by at least amino acid residues 173, 176,

177, 178, 179, 180, 236, 237, 238, 239, 244, 248, 283, 284, 285, 290, 338, 339, 340, 341, 342, 343, 344, 345, 348, 352, 381 and 383, using the sequence and numbering according to Thornberry et al., supra (SEQ ID NO:1).

The term "accessory binding site" or "accessory binding site moiety" refers to a binding site of ICE comprising amino acid residues adjacent to the two-fold axis of ICE but external to the active site, according to Table A. An accessory binding site may be a locus of ICE inhibition, although it is not the site of substrate cleavage.

The accessory binding site is characterized by at least amino acid residues 150, 151, 240, 259, 267, 268, 274, 291, 292, 293, 294, 295, 296, 297, 317, 318, 319, 320, 321, 322, 323, 324, 325, 327, 334, 335, 367, 371, 374, 375, 377, 378, 380, 382, 384, 386, 388, 389, 390, 391, 392, 393, 394, 395 and 396, using the sequence and numbering according to Thornberry et al., supra (SEQ ID NO:1).

The term "P binding pocket" refers to a binding subsite, or portion of the binding site on the ICE molecule. The amino acid residues of an ICE substrate are given designations according to their position relative to the scissile bond, i.e. the bond that is broken by the protease. Residues are designated P1, P2, etc., for those extending toward the N-terminus from the scissile bond of the substrate. The residues are designated P1', P2', etc., for those extending toward the C-terminus from the scissile bond of the substrate.

The portions of an ICE inhibitor that correspond to the P or P' residues of the substrate are also labeled P1, P1', etc., by analogy with the substrate. The binding subsites of the ICE molecule that receive the residues labeled P1, P1', etc., are

designated "the S1 site", "the P1' binding pocket", etc. Schechter, I. and A. Berger, "On the Size of the Active Site in Proteases", Biochem. Biophys. Res. Commun., 27, pp. 157-162 (1967).

The "P1 binding pocket" of the ICE active site is defined as the space surrounded by amino acid residues Arg-179, His-237, Gln-283 and Arg-341.

The "P2 binding pocket" of the ICE active site is defined as the space surrounded by amino acid residues Pro-290, Val-338 and Trp-340.

The "P3 binding pocket" of the ICE active site is defined as the space surrounded by amino acid residues Pro-177, Arg-178, Thr-180, Arg-341 and Pro-343.

The "P4 binding pocket" of the ICE active site is defined as the space surrounded by amino acid residues Trp-340, His-342, Met-345, Val-348, Arg-352, Asp-381 and Arg-383.

The "P' binding pocket" of the ICE active site is defined as the space surrounded by amino acid residues Phe-173, Ile-176, His-237, Gly-238, Ile-239, Cys-244 and His-248.

The term "p10 subunits interacting across the two-fold axis" means having at least 50% of the interface contacts according to Table A.

The term "structure coordinates" refers to mathematical coordinates derived from mathematical equations related to the patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centers) of an ICE molecule in crystal form. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are used to establish the positions of the individual atoms within the unit cell of the crystal.

The term "heavy atom derivatization" refers to the method of producing a chemically modified form of a crystal of ICE. In practice, a crystal is soaked in a solution containing heavy metal atom salts, or organometallic compounds, e.g., lead chloride, gold thiomalate, thimerosal or uranyl acetate, which can diffuse through the crystal and bind to the surface of the protein. The location(s) of the bound heavy metal atom(s) can be determined by X-ray diffraction analysis of the soaked crystal. This information, in turn, is used to generate the phase information used to construct three-dimensional structure of the enzyme. Blundel, T.L. and N.L. Johnson, Protein Crystallography, Academic Press (1976).

Those of skill in the art understand that a set of structure coordinates determined by X-ray crystallography is not without standard error. For the purpose of this invention, any set of structure coordinates for ICE or ICE homologues or ICE mutants that have a root mean square deviation of protein backbone atoms (N, Cα, C and O) of less than 0.75Å when superimposed -- using backbone atoms -- on the structure coordinates listed in Table B shall be considered identical.

The term "unit cell" refers to a basic parallelipiped shaped block. The entire volume of a crystal may be constructed by regular assembly of such blocks. Each unit cell comprises a complete representation of the unit of pattern, the repetition of which builds up the crystal.

The term "space group" refers to the arrangement of symmetry elements of a crystal.

The term "molecular replacement" refers to a method that involves generating a preliminary model of an ICE crystal whose structure coordinates are unknown,

by orienting and positioning a molecule whose structure coordinates are known (e.g., ICE coordinates from Table B) within the unit cell of the unknown crystal so as best to account for the observed diffraction pattern of the unknown crystal. Phases can then be calculated from this model and combined with the observed amplitudes to give an approximate Fourier synthesis of the structure whose coordinates are unknown. This, in turn, can be subject to any of the several forms of refinement to provide a final, accurate structure of the unknown crystal. Lattman, E., "Use of the Rotation and Translation Functions", in Methods in Enzymology, 115, pp. 55-77 (1985); M.G. Rossmann, ed., "The Molecular Replacement Method", Int. Sci. Rev. Ser., No. 13, Gordon & Breach, New York, (1972). Using the structure coordinates of ICE provided by this invention, molecular replacement may be used to determine the structure coordinates of a crystalline mutant or homologue of ICE or of a different crystal form of ICE.

DETAILED DESCRIPTION OF THE INVENTION

In order that the invention described herein may be more fully understood, the following detailed description is set forth.

The present invention relates to crystalline interleukin-1ß converting enzyme ("ICE"), the structure of ICE as determined by X-ray crystallography, the use of that structure to solve the structure of ICE homologues and of other crystal forms of ICE, mutants and co-complexes of ICE, and the use of the ICE structure and that of its homologues, mutants and co-complexes to design inhibitors of ICE.

A. The Structure of ICE

The present invention provides, for the first time, crystals of human ICE grown in the presence of a tetrapeptide inhibitor from solutions of polyethylene glycol, as well as the structure of ICE as determined therefrom. The crystals have tetragonal space group symmetry $P4_32_12$. The unit cell of said crystals has a rectangular shape of dimensions a=b=65 ± 5Å, and c=162 ± 5Å. The structure coordinates of ICE, as determined by X-ray crystallography of crystalline ICE, are listed in Table B.

Crystal packing reveals that ICE is a $(p20)_2/(p10)_2$ tetramer. In the tetramer, two p20 subunits contact two adjacent p10 subunits which interact across the crystallographic two-fold axis (Figure 2). This axis corresponds to an oligomer interface in solution. Most of the dimer-dimer interface consists of p20 residues 291-297 and of p10 residues 318-322 and 386-396.

Figure 1 represents a ribbon drawing of the p20/p10 ICE heterodimer. As depicted in the figure, the p20 and p10 subunits are intimately associated and the active site is at the top of the figure, roughly at the center of the cluster of displayed side chains.

The enzyme core is a six-stranded ß-sheet with 5 parallel strands (numbered 1, 2, 3, 4 and 7) and one anti-parallel strand (numbered 8). Six α-helices (lettered A, B, C, D, E and F) lie roughly parallel to the ß-strands. The last seven residues of p20 and the first seven of p10 protrude from this compact structure and form two anti-parallel ß-strands [5 (residues 291-297)] and 6 (residues 317-323)]. A few key residues are labelled according to their position in the p45 amino acid sequence of ICE (Thornberry et al., supra).

Our understanding of the structure of ICE has enabled, for the first time, identification of the active site and accessory binding site of the enzyme. The p10 subunit from one ICE molecule contacts the p20 subunit from a different molecule and together they create an active site. The active site spans both the p20 and p10 subunits and comprises amino acid residues from both subunits. The active site moiety is characterized by at least amino acid residues 173, 176, 177, 178, 179, 180, 236, 237, 238, 239, 244, 248, 283, 284, 285, 290, 338, 339, 340, 341, 342, 343, 344, 345, 348, 352, 381 and 383 using the sequence numbering according to Thornberry et al., supra (SEQ ID NO:1).

An accessory binding site is formed by amino acid residues on the p10 subunits that interact across the two-fold axis. The accessory binding site moiety is characterized by at least amino acid residues 150, 151, 240, 259, 267, 268, 274, 291, 292, 293, 294, 295, 296, 297, 317, 318, 319, 320, 321, 322, 323, 324, 325, 327, 334, 335, 367, 371, 374, 375, 377, 378, 378, 380, 382, 384, 386, 388, 389, 390, 391, 392, 393, 394, 395 and 396 using the sequence numbering according to Thornberry et al., supra (SEQ ID NO:1).

B. Uses of the Structure Coordinates of ICE

For the first time, the present invention permits the use of molecular design techniques to design, select and synthesize chemical entities and compounds, including inhibitory compounds, capable of binding to the active site or accessory binding site of ICE, in whole or in part.

On approach enabled by this invention, is to use the structure coordinates of ICE to design compounds that bind to the enzyme and alter the physical properties of the compounds in different ways,

e.g., solubility. For example, this invention enables the design of compounds that act as competitive inhibitors of the ICE enzyme by binding to, all or a portion of, the active site of ICE. This invention also enables the design of compounds that act as uncompetitive inhibitors of the ICE enzyme. These inhibitors may bind to, all or a portion of, the accessory binding site of an ICE already bound to its substrate and may be more potent and less non-specific than known competitive inhibitors that compete only for the ICE active site. Similarly, non-competitive inhibitors that bind to and inhibit ICE whether or not it is bound to another chemical entity may be designed using the structure coordinates of ICE of this invention.

A second design approach is to probe an ICE crystal with molecules composed of a variety of different chemical entities to determine optimal sites for interaction between candidate ICE inhibitors and the enzyme. For example, high resolution X-ray diffraction data collected from crystals saturated with solvent allows the determination of where each type of solvent molecule sticks. Small molecules that bind tightly to those sites can then be designed and synthesized and tested for their ICE inhibitor activity. Travis, J., Science, 262, p. 1374 (1993).

This invention also enables the development of compounds that can isomerize to short-lived reaction intermediates in the chemical reaction of a substrate or other compound that binds to ICE, with ICE. Thus, the time-dependent analysis of structural changes in ICE during its interaction with other molecules is enabled. The reaction intermediates of ICE can also be deduced from the reaction product in co-complex with ICE. Such information is useful to design improved

analogues of known ICE inhibitors or to design novel classes of inhibitors based on the reaction intermediates of the ICE enzyme and ICE-inhibitor co-complex. This provides a novel route for designing ICE inhibitors with both high specificity and stability.

Another approach made possible and enabled by this invention, is to screen computationally small molecule data bases for chemical entities or compounds that can bind in whole, or in part, to the ICE enzyme. In this screening, the quality of fit of such entities or compounds to the binding site may be judged either by shape complementarity or by estimated interaction energy. Meng, E.C. et al., J. Comp. Chem., 13, pp. 505-524 (1992).

Because ICE may crystallize in more than one crystal form, the structure coordinates of ICE, or portions thereof, as provided by this invention are particularly useful to solve the structure of those other crystal forms of ICE. They may also be used to solve the structure of ICE mutants, ICE co-complexes, or of the crystalline form of any other protein with significant amino acid sequence homology to any functional domain of ICE.

One method that may be employed for this purpose is molecular replacement. In this method, the unknown crystal structure, whether it is another crystal form of ICE, an ICE mutant, or an ICE co-complex, or the crystal of some other protein with significant amino acid sequence homology to any functional domain of ICE, may be determined using the ICE structure coordinates of this invention as provided in Table B. This method will provide an accurate structural form for the unknown crystal more quickly and efficiently than attempting to determine such information *ab initio*.

In addition, in accordance with this invention, ICE mutants may be crystallized in co-complex with known ICE inhibitors. The crystal structures of a series of such complexes may then be solved by molecular replacement and compared with that of wild-type ICE. Potential sites for modification within the various binding sites of the enzyme may thus be identified. This information provides an additional tool for determining the most efficient binding interactions, for example, increased hydrophobic interactions, between ICE and a chemical entity or compound.

All of the complexes referred to above may be studied using well-known X-ray diffraction techniques and may be refined versus 2-3Å resolution X-ray data to an R value of about 0.20 or less using computer software, such as X-PLOR (Yale University, ©1992, distributed by Molecular Simulations, Inc.). See, e.g., Blundel & Johnson, supra; Methods in Enzymology, vol. 114 & 115, H.W. Wyckoff et al., eds., Academic Press (1985). This information may thus be used to optimize known classes of ICE inhibitors, and more importantly, to design and synthesize novel classes of ICE inhibitors.

The structure coordinates of ICE mutants provided in this invention also facilitate the identification of related proteins or enzymes analogous to ICE in function, structure or both, thereby further leading to novel therapeutic modes for treating or preventing IL-1 mediated diseases.

The design of compounds that bind to or inhibit ICE according to this invention generally involves consideration of two factors. First, the compound must be capable of physically and structurally associating with ICE. Non-covalent molecular

interactions important in the association of ICE with its substrate include hydrogen bonding, van der Waals and hydrophobic interactions.

Second, the compound must be able to assume a conformation that allows it to associate with ICE. Although certain portions of the compound will not directly participate in this association with ICE, those portions may still influence the overall conformation of the molecule. This, in turn, may have a significant impact on potency. Such conformational requirements include the overall three-dimensional structure and orientation of the chemical entity or compound in relation to all or a portion of the binding site, e.g., active site or accessory binding site of ICE, or the spacing between functional groups of a compound comprising several chemical entities that directly interact with ICE.

The potential inhibitory or binding effect of a chemical compound on ICE may be analyzed prior to its actual synthesis and testing by the use of computer modelling techniques. If the theoretical structure of the given compound suggests insufficient interaction and association between it and ICE, synthesis and testing of the compound is obviated. However, if computer modelling indicates a strong interaction, the molecule may then be synthesized and tested for its ability to bind to ICE and inhibit using the fluorescent substrate assay of Thornberry et al., supra. In this manner, synthesis of inoperative compounds may be avoided.

An inhibitory or other binding compound of ICE may be computationally evaluated and designed by means of a series of steps in which chemical entities or fragments are screened and selected for their

ability to associate with the individual binding pockets or other areas of ICE.

One skilled in the art may use one of several methods to screen chemical entities or fragments for their ability to associate with ICE and more particularly with the individual binding pockets of the ICE active site or accessory binding site. This process may begin by visual inspection of, for example, the active site on the computer screen based on the ICE coordinates in Table B. Selected fragments or chemical entities may then be positioned in a variety of orientations, or docked, within an individual binding pocket of ICE as defined supra. Docking may be accomplished using software such as Quanta and Sybyl, followed by energy minimization and molecular dynamics with standard molecular mechanics forcefields, such as CHARMM and AMBER.

Specialized computer programs may also assist in the process of selecting fragments or chemical entities. These include:

1. GRID (Goodford, P.J., "A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules", J. Med. Chem., 28, pp. 849-857 (1985)). GRID is available from Oxford University, Oxford, UK.

2. MCSS (Miranker, A. and M. Karplus, "Functionality Maps of Binding Sites: A Multiple Copy Simultaneous Search Method." Proteins: Structure, Function and Genetics, 11, pp. 29-34 (1991)). MCSS is available from Molecular Simulations, Burlington, MA.

3. AUTODOCK (Goodsell, D.S. and A.J. Olsen, "Automated Docking of Substrates to Proteins by Simulated Annealing", Proteins: Structure, Function, and Genetics, 8, pp. 195-202 (1990)). AUTODOCK is available from Scripps Research Institute, La Jolla, CA.

4. DOCK (Kuntz, I.D. et al., "A Geometric Approach to Macromolecule-Ligand Interactions", J. Mol. Biol., 161, pp. 269-288 (1982)). DOCK is

available from University of California, San Francisco, CA.

Once suitable chemical entities or fragments have been selected, they can be assembled into a single compound or inhibitor. Assembly may be proceed by visual inspection of the relationship of the fragments to each other on the three-dimensional image displayed on a computer screen in relation to the structure coordinates of ICE. This would be followed by manual model building using software such as Quanta or Sybyl.

Useful programs to aid one of skill in the art in connecting the individual chemical entities or fragments include:

1. CAVEAT (Bartlett, P.A. et al, "CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules". In Molecular Recognition in Chemical and Biological Problems", Special Pub., Royal Chem. Soc., 78, pp. 182-196 (1989)). CAVEAT is available from the University of California, Berkeley, CA.

2. 3D Database systems such as MACCS-3D (MDL Information Systems, San Leandro, CA). This area is reviewed in Martin, Y.C., "3D Database Searching in Drug Design", J. Med. Chem., 35, pp. 2145-2154 (1992)).

3. HOOK (available from Molecular Simulations, Burlington, MA).

Instead of proceeding to build an ICE inhibitor in a step-wise fashion one fragment or chemical entity at a time as described above, inhibitory or other ICE binding compounds may be designed as a whole or "de novo" using either an empty active site or optionally including some portion(s) of a known inhibitor(s). These methods include:

1. LUDI (Bohm, H.-J., "The Computer Program LUDI: A New Method for the De Novo Design of Enzyme Inhibitors", J. Comp. Aid. Molec. Design, 6, pp. 61-78 (1992)). LUDI is available from Biosym Technologies, San Diego, CA.

2. LEGEND (Nishibata, Y. and A. Itai, Tetrahedron, 47, p. 8985 (1991)). LEGEND is available from Molecular Simulations, Burlington, MA.

3. LeapFrog (available from Tripos Associates, St. Louis, MO).

Other molecular modelling techniques may also be employed in accordance with this invention. See, e.g., Cohen, N.C. et al., "Molecular Modeling Software and Methods for Medicinal Chemistry, J. Med. Chem., 33, pp. 883-894 (1990). See also, Navia, M.A. and M.A. Murcko, "The Use of Structural Information in Drug Design", Current Opinions in Structural Biology, 2, pp. 202-210 (1992).

Once a compound has been designed or selected by the above methods, the efficiency with which that compound may bind to ICE may be tested and optimized by computational evaluation. For example, a compound that has been designed or selected to function as an ICE-inhibitor must also preferably traverse a volume not overlapping that occupied by the active site when it is bound to the native substrate. An effective ICE inhibitor must preferably demonstrate a relatively small difference in energy between its bound and free states (i.e., a small deformation energy of binding). Thus, the most efficient ICE inhibitors should preferably be designed with a deformation energy of binding of not greater than about 10 kcal/mole, preferably, not greater than 7 kcal/mole. ICE inhibitors may interact with the enzyme in more than one conformation that is similar in overall binding energy. In those cases, the deformation energy of binding is taken to be the difference between the energy of the free compound and the average energy of the conformations observed when the inhibitor binds to the enzyme.

A compound designed or selected as binding to ICE may be further computationally optimized so that in its bound state it would preferably lack repulsive electrostatic interaction with the target enzyme. Such non-complementary (e.g., electrostatic) interactions include repulsive charge-charge, dipole-dipole and charge-dipole interactions. Specifically, the sum of all electrostatic interactions between the inhibitor and the enzyme when the inhibitor is bound to ICE, preferably make a neutral or favorable contribution to the enthalpy of binding.

Specific computer software is available in the art to evaluate compound deformation energy and electrostatic interaction. Examples of programs designed for such uses include: Gaussian 92, revision C [M.J. Frisch, Gaussian, Inc., Pittsburgh, PA ©1992]; AMBER, version 4.0 [P.A. Kollman, University of California at San Francisco, ©1994]; QUANTA/CHARMM [Molecular Simulations, Inc., Burlington, MA ©1994]; and Insight II/Discover (Biosysm Technologies Inc., San Diego, CA ©1994). These programs may be implemented, for instance, using a Silicon Graphics workstation, IRIS 4D/35 or IBM RISC/6000 workstation model 550. Other hardware systems and software packages will be known to those skilled in the art.

Once an ICE-binding compound has been optimally selected or designed, as described above, substitutions may then be made in some of its atoms or side groups in order to improve or modify its binding properties. Generally, initial substitutions are conservative, i.e., the replacement group will have approximately the same size, shape, hydrophobicity and charge as the original group. It should, of course, be understood that components known in the art to alter conformation should be avoided. Such substituted

chemical compounds may then be analyzed for efficiency of fit to ICE by the same computer methods described in detail, above.

C. Mutants Of ICE

The present invention also enables mutants of ICE and the solving of their crystal structure. More particularly, by virtue of the present invention, the location of the active site, accessory binding site and interface of ICE based on its crystal structure permits the identification of desirable sites for mutation.

For example, mutation may be directed to a particular site or combination of sites of wild-type ICE, i.e., the accessory binding site or only the active site, or a location on the interface site may be chosen for mutagenesis. Similarly, only a location on, at or near the enzyme surface may be replaced, resulting in an altered surface charge of one or more charge units, as compared to the wild-type enzyme. Alternatively, an amino acid residue in ICE may be chosen for replacement based on its hydrophilic or hydrophobic characteristics.

Such mutants may be characterized by any one of several different properties as compared with wild-type ICE. For example, such mutants may have altered surface charge of one or more charge units, or have an increased stability to subunit dissociation. Or such mutants may have an altered substrate specificity in comparison with, or a higher specific activity than, wild-type ICE.

The mutants of ICE prepared by this invention may be prepared in a number of ways. For example, the wild-type sequence of ICE may be mutated in those sites identified using this invention as desirable for mutation, by means of oligonucleotide-directed

mutagenesis or other conventional methods, e.g. deletion. Alternatively, mutants of ICE may be generated by the site specific replacement of a particular amino acid with an unnaturally occurring amino acid. In addition, ICE mutants may be generated through replacement of an amino acid residue, or a particular cysteine or methionine residue, with selenocysteine or selenomethionine. This may be achieved by growing a host organism capable of expressing either the wild-type or mutant polypeptide on a growth medium depleted of either natural cysteine or methionine (or both) but enriched in selenocysteine or selenomethionine (or both).

Mutations may be introduced into a DNA sequence coding for ICE using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired mutation sites. Mutations may be generated in the full-length DNA sequence of ICE (p45) or in any sequence coding for p30, or p20 or p10 polypeptides.

According to this invention, a mutated ICE DNA sequence produced by the methods described above, or any alternative methods known in the art, can be expressed using an expression vector. An expression vector, as is well known in the art, typically includes elements that permit autonomous replication in a host cell independent of the host genome, and one or more phenotypic markers for selection purposes. Either prior to or after insertion of the DNA sequences surrounding the desired ICE mutant coding sequence, an expression vector also will include control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes and a signal for termination. In some embodiments, where secretion

of the produced mutant is desired, nucleotides encoding a "signal sequence" may be inserted prior to the ICE mutant coding sequence. For expression under the direction of the control sequences, a desired DNA sequence must be operatively linked to the control sequences -- i.e., they must have an appropriate start signal in front of the DNA sequence encoding the ICE mutant and maintaining the correct reading frame to permit expression of that sequence under the control of the control sequences and production of the desired product encoded by that ICE sequence.

Any of a wide variety of well known available expression vectors are useful to express the mutated ICE coding sequences of this invention.

These include, for example, vectors consisting of segments of chromosomal, non-chromosomal and synthetic DNA sequences, such as various known derivatives of SV40, known bacterial plasmids, e.g., plasmids from E. coli including col E1, pCR1, pBR322, pMB9 and their derivatives, wider host range plasmids, e.g., RP4, phage DNAs, e.g., the numerous derivatives of phage λ, e.g., NM 989, and other DNA phages, e.g., M13 and filamentous single stranded DNA phages, yeast plasmids such as the 2μ plasmid or derivatives thereof, and vectors derived from combinations of plasmids and phage DNAs, such as plasmids which have been modified to employ phage DNA or other expression control sequences. In the preferred embodiments of this invention, we employ E. coli vectors.

In addition, any of a wide variety of expression control sequences -- sequences that control the expression of a DNA sequence when operatively linked to it -- may be used in these vectors to express the mutated DNA sequences according to this invention. Such useful expression control sequences, include, for

example, the early and late promoters of SV40 for animal cells, the lac system, the trp system the TAC or TRC system, the major operator and promoter regions of phage λ the control regions of fd coat protein, all for E. coli, the promoter for 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase, e.g., Pho5, the promoters of the yeast α-mating factors for yeast, and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells or their viruses, and various combinations thereof. In the preferred embodiments of this invention, we employ either E. coli or eukaryotic expression in COS-1 cells, a monkey kidney cell line.

A wide variety of hosts are also useful for producing mutated ICE according to this invention. These hosts include, for example, bacteria, such as E. coli, Bacillus and Streptomyces, fungi, such as yeasts, and animal cells, such as CHO and COS-1 cells, plant cells and transgenic host cells. In preferred embodiments of this invention, the host cells are E. coli or COS-1 cells.

It should be understood that not all expression vectors and expression systems function in the same way to express mutated DNA sequences of this invention and to produce modified ICE or ICE mutants. Neither do all hosts function equally well with the same expression system. However, one of skill in the art may make a selection among these vectors, expression control sequences and hosts without undue experimentation and without departing from the scope of this invention. For example, an important consideration in selecting a vector, will be the ability of the vector to replicate in a given host. The copy number of the vector, the ability to control that copy number, and the expression of any other

proteins encoded by the vector, such as antibiotic markers, should also be considered.

In selecting an expression control sequence, a variety of factors should also be considered. These include, for example, the relative strength of the system, its controllability, its compatibility with the DNA sequence encoding the modified ICE of this invention, particularly with regard to potential secondary structures.

Hosts should be selected by consideration of their compatibility with the chosen vector, the toxicity of the modified ICE to them, their ability to secrete mature products, their ability to fold proteins correctly, and to form tetramers, their fermentation requirements, the ease of the purification of the modified ICE from them and safety. Within these parameters, one of skill in the art may select various vector/expression control system/host combinations that will produce useful amounts of the mutant ICE.

The mutant ICE produced in these systems may be purified by a variety of conventional steps and strategies, including those used to purify wild-type ICE.

Once the ICE mutants have been generated in the desired location, i.e., active site or accessory binding site, the mutants may be tested for any one of several properties of interest.

For example, mutants may be screened for an altered charge at physiological pH. This is determined by measuring the mutant ICE isoelectric point (pI) in comparison with that of the wild-type parent. Isoelectric point may be measured by gel-electrophoresis according to the method of Wellner, D., Analyt. Chem., 43, p. 597 (1971). A mutant with an altered surface charge is an ICE polypeptide containing

a replacement amino acid located at the surface of the enzyme, as provided by the structural information of this invention, and an altered pI.

Furthermore, mutants may be screened for high specific activity in relation to the wild-type ICE. A mutant would demonstrate high specific activity if its second order rate constant (K_{cat}/K_m) for hydrolysis of the substrate Ac-Tyr-Val-Ala-Asp-amino methylcoumarin exceeds 7×10^4 $M^{-1}s^{-1}$ at 25°C, using the assay in Pennington & Thornberry, supra.

A mutant would be tested for altered ICE substrate specificity by measuring the hydrolysis of fluorgenic peptide substrates or unmodified ICE peptide substrates as described in Thornberry et al., supra. An enzyme with altered substrate specificity is an enzyme whose second order rate constant (k_{cat}/K_m) for a substrate X_1-Tyr-Val-Ala-X_2-X_3 that exceeds the k_{cat}/K_m for the analogous peptide substrate X_1-Tyr-Val-Ala-Asp-X_3. X_1 is an amino protecting group, such as acetyl; X_2 is a natural or unnatural amino acid residue other than L-aspartate; X_3 is a carboxyl protecting group such as aminomethylcoumarin or p-nitroaniline.

Further properties of interest also include mutants with increased stability to subunit dissociation. An ICE mutant with increased stability to subunit dissociation would demonstrate no loss of enzymic activity at concentrations of the enzyme below 10 nM in comparison with the wild-type ICE, which demonstrates a Kd between 1-10 nM.

In order that the invention described herein may be more fully understood, the following examples are set forth. It should be understood that these examples are for illustrative purposes only and are not to be construed as limiting this invention in any manner.

EXAMPLE 1

Crystal Structure of ICE

The cDNA encoding the p30 precursor of active human ICE (residues Asn 120 to His 404 of p45 (Thornberry et al., supra]) was cloned into a P_L promoter expression vector (provided by Dr. J. Mankovich) and expressed in E. coli by temperature-shift induction.

Pre-induction repression of the P_L promoter was achieved by co-expression of the cI repressor gene on a co-resident, compatible plasmid (pACYC184cI) in the E. coli host, JM109. Yanish-Perron, C., et al., Gene, 33, pp. 103-199 (1985; ATCC #53323). The promoter was induced by increasing the temperature from 28°C to 42°C, at which point the temperature sensitive cI repressor gene product denatures and gene expression is initiated, directed by the P_L promoter. Maintenance of the temperature at 42°C for a further 4 hours resulted in the accumulation of high levels of the inactive ICE p30 precursor product within the host cell cytoplasm, in the form of inactive inclusion bodies.

After mechanical disruption of the cells, and harvesting of the insoluble fraction, the inclusion bodies were washed by suspension in 2M urea, 25mM tris, 0.5mM DTT, 0.1mM EDTA, 0.1mM PMSF, pH 7.5 at 4°C, followed by centrifugation. The inclusion bodies were solubilized in the above buffer containing 7M urea, centrifuged and subjected to size-exclusion chromatography in the same buffer. The p30 fractions, identified by SDS-PAGE and N-terminal sequence analysis, were pooled and diluted to 0.3 mg/ml using column buffer. This was followed by dialysis at 4°C against 25mM tris, 1mM DTT, pH 7.5, until the urea

concentration was less than 20mM, thereby allowing the enzyme to refold.

The protein was concentrated to 3-5 mg/ml by ultrafiltration at 4°C, followed by incubation at room temperature. The disappearance of the p30 precursor, and the concomitant appearance of the p20 and p10 subunits, was monitored by SDS-PAGE, evidence that autocatalytic processing of the enzyme had occurred. ICE enzymatic activity was assayed by hydrolysis of a Succinyl-Tyr-Val-Ala-Asp-p-nitroanilide substrate at 37°C and correlated closely with conversion to subunits.

The autoprocessed ICE was inhibited fully by adding a 2x molar excess of a tetrapeptide aldehyde inhibitor (acetyl-Tyr-Val-Ala-Asp-H). The protein-inhibitor complex sample was concentrated and fractionated by size-exclusion chromatography, in final preparation for crystallization experiments.

Crystals of ICE in complex with the inhibitor were grown by vapor diffusion. Davies, D.R. and D.M. Segal, Meth. Enzymol., 22, p. 266 (1971). Protein (20 mg/ml in 50 mM citrate, 2.0 mM DTT, pH 6.5) was mixed with an equal volume of reservoir buffer (15% (w/v) PEG 4K, 400 mM $LiSO_4$, 200 mM sodium Hepes, 5mM sodium cacodylate, 0.5% beta-octyl glucoside, pH 7.0) and allowed to stand over the reservoir solution at 4°C. Crystals grew over a six week period to form tetragonal bipyramids and were equilibrated with 18% PEG 4K, 400 mM $LiSO_4$, 200 mM sodium Hepes, 5mM sodium cacodylate, 0.5% beta-octyl glucoside, pH 7.0 prior to data collection or heavy atom derivatization.

Those of skill in the art will appreciate that the aforesaid crystallization conditions can be varied. Such variations may be used alone or in combination, and include final protein/inhibitor

complex concentrations between 5 mg/ml and 35 mg/ml; all combinations of ICE/inhibitor to precipitant ratios; citrate concentrations between 1mM and 200 mM; DTT concentrations between 0 mM and 10 mM; and any concentration of ß-mercaptoethanol; pH ranges between 5.5 and 9.5; PEG concentrations between 10% and 25% (gms/100ml); PEG weights between 2000 and 8000; $LiSO_4$ concentrations between 50 and 750 mM; HEPES concentrations between 5 and 395 mM; and any concentration or type of detergent; any temperature between -5°C and 30°C; and crystallization of ICE/inhibitor complexes by batch, liquid bridge, or dialysis method using these conditions or variations thereof.

All X-ray data sets were collected on a R-axis IIC image plate system except for the 2.2Å Synchrotron data set that was used for refinement of the final model. This data was collected at Cornell High Energy Synchrotron Source ("CHESS") on a charge-couple device and was reduced to structure factor amplitudes using the Denzo Software Package (Denzo - An Oscillation Data Processing Program For Macro Molecular Crystallography, ©1993, Daniel Gewirth, Yale University). Oscillation photographs were integrated and reduced to structure factor amplitudes using software supplied by the manufacturer (Molecular Structures Corp., Dallas, Texas).

Refined heavy atom parameters were used to compute multiple isomorphous replacement phases. Inclusion of the anomalous data for the Hg derivative in cross-phased difference Fourier maps showed the space group to be $P4_32_12$ rather than its enantiomorph. The mean figure of merit, including anomalous data for the Hg derivative, was 0.65 to 3.5Å resolution (Table 1).

Solvent flattening and phase extension (CCP4-Collaborative Computing Project No. 4, A Suite of Programs for Protein Crystallography; Daresbury Laboratory, Warrington, WA4 4AD, U.K. (1979)) improved the map and allowed identification of some of the residues in the protein core. Cycles of model building (Quanta, version 4.0b, Molecular.Simulations Inc., Burlington MA), positional refinement, (Brunger, A.T., J. Acta Cryst., A46, pp. 46-57 (1990); Brunger, A.T. et al., J. Acta Cryst., A46, pp. 585-93 (1990)) and phase combination (CCP4-Collaborative Computing Project, supra) were carried out until the switch to phases calculated from the model could be made. Refinement continued against the -16°C, 2.2Å data (Table 1), which allowed the more difficult loop regions of the protein to be constructed.

The following table summarizes the X-ray crystallography data sets of ICE derivatives that were used to determine the structure of ICE according to this invention.

Table 1

Protein Modification	Resolution Å	Completeness of data %	Rmerge %	Unit cell dimensions, Å a,b	c	No. of sites	Rc %	Phasing Power
Tetrapeptide aldehyde*	20 - 2.2	87	7.1	64.9	164.1	--	--	--
Tetrapeptide aldehyde**	20 - 2.6	90	8.3	64.4	163.3	--	--	--
Tetrapeptide aldehyde	20 - 2.8	78	8.3	64.7	162.9	--	--	--
Iodinated tetrapeptide aldehyde	20 - 3.5	86	9.4	64.4	162.8	2	0.88	1.09
Thimerosal	20 - 3.5	88	8.4	64.4	162.3	5	0.67	1.08
Gold Thiomalate	20 - 3.5	74	9.5	64.7	162.7	3	0.72	1.22
Uranyl Acetate	20 - 4.0	80	10.8	64.7	162.9	2	0.79	1.32
Lead Chloride	20 - 3.5	64	8.9	64.7	162.8	2	0.76	1.38

* Data collected at -16°C at CHESS

** Data collected at -16°C

Definitions: Rmerge gives the agreement between repeated intensity measurements, with the number of crystals used in the data set given in parentheses. The number of heavy-atom binding sites is given where

appropriate. R_c is the Cullis R factor for centrosymmetric reflections, and the phasing power is the ratio of average heavy-atom scattering to the average lack of closure of the phase triangles. Blundell, T.L. and Johnson, L.N., Protein Crystallography, Academic Press, New York (1976).

The ICE tetrameric model according to this invention has an R-factor of 19% against all observed data between 7Å and 2.2Å resolution, with root-mean-square deviation from ideal bond lengths and angles of 0.011Å and 2.84Å respectively.

EXAMPLE 2

Confirmation of the Active Site of ICE

In order to confirm the location of the active site in the tetrameric ICE molecule, as deduced from the structure coordinates of ICE, a series of p30 ICE mutants was generated.

Oligonucleotide-directed mutagenesis was performed on pcDNA3 (Invitrogen) constructs using uracil-enrichment of single-strand DNA. Kunkel, T.A., Proc. Nat. Acad. Sci., 82, pp. 488-492 (1985); Kunkel, T.A. et al., Meth. Enzymol., 154, pp. 367-382 (1987). This is a modification of the method originally described for M13 mutagenesis. Zoller, M.J. and M. Smith, Nucleic Acids Res., 10, pp. 6487-6500 (1983); Zoller M.J. and M. Smith, Meth. Enzymol., 100, pp. 468-500 (1983).

Mutagenesis was performed using the reagents provided in the Muta-Gene Kit (BioRad). Mutagenesis primers were synthesized in the (+) coding orientation. The dut^-ung^- *E. coli* strain CJ326 was used for uracil enrichment of single-strand DNA, and the MV1190 strain was used for selection of heteroduplex DNA after extension-ligation reactions. All oligonucleotides

were synthesized on an applied Biosystems 380 DNA synthesizer and purified by electrophoreses in polyacrylamide-urea slab gels. Mutations made in the 30kDa ICE-encoding cDNA were fully sequenced in the coding region by the dideoxy method. Sanger, F. et al., Proc. Nat. Acad. Sci. 74, pp. 5463-5467 (1977). Mutant DNA in preparation for COS-1 cell transfection, or alternatively *E. coli* transfection, was purified by alkaline lysis and cesium gradient centrifugation prior to transfection.

Each mutant cDNA was transfected into a COS-1 cell line, then tested for its ability to process pIL-1ß *in vitro*, i.e., to secrete mature IL-1ß. The COS-1 cell line used, had previously been transfected with a pIL-1ß encoding cDNA cloned into an MNC stuffer vector (B. Seed, Harvard Medical School) which had subsequently integrated into the chromosome. pIL-1ß production was maintained by the addition of 0.5 mg/ml G-418 Sulfate to culture media.

Approximately 3 x 10^6 COS-1 cells in 100mm tissue culture plates were transfected with 15 μg of each plasmid. DNA was mixed with 200 μl DEAE-Dextran, brought to 4 ml with phosphate-buffered saline, and added to the plates. Cells were incubated at 37°C for 30 min. 8 ml of an 80 μM chloroquine/serum-free DMEM solution was added and the cells were incubated for 2.5 hr. This solution was aspirated and cells were treated for two minutes with 10% DMSO/serum-free DMEM. After washing with serum-free media, 10 ml complete media was added. Conditioned media were sampled at 16 and 24 hr. Activity in this assay requires that transcription, translation and protein folding of mutants are not arrested. The amount of mutant ICE present in cell lysates was determined by Western blot using an anti-p20 rabbit antiserum that recognizes

amino acids 136-150 inclusive and which also recognizes the intact p30 precursor.

Mature IL-1ß in the cell medium was detected by ELISA (R&D Systems). Samples were diluted to achieve concentrations in the linear range of the ELISA assay (8-60 pg/ml). Background IL-1ß levels were determined in cells transfected with the expression vector lacking ICE cDNA, and this value was subtracted from all other concentrations. The % activity values were calculated as the ratio of secreted IL-1ß from cells transfected with mutant ICE divided by IL-1ß secreted by cells transfected with wild-type ICE. The final ratio is the mean of at least two experiments. These data are recorded in Figure 3.

Based on these data, it was determined that mutation of Cys-285 or His-237 eliminates pIL-1ß processing activity, as well as autoprocessing. Mutation of Arg-179, which contacts the P1 Asp to Glu, also abolishes activity. Mutation of Cys-244 to Ala, which may contact P' side chains of substrates, reduces enzymatic activity significantly. In contrast, mutation of other residues proximal to Cys-285 including Ser-332, -333 or -339, and His-249, does not eliminate activity. Accordingly, we confirmed the importance of various residues in the ICE active site.

EXAMPLE 3

The Use of Molecular Replacement To Solve An Unknown ICE Crystal Structure

The method of molecular replacement was used to determine the structure coordinates of crystals of ICE in complex with the tetrapeptide aldehyde inhibitor Ac-Tyr-Val-Pro-Asp-H in comparison with crystals of ICE in complex with the tetrapeptide aldehyde inhibitor Ac-Tyr-Val-Ala-Asp-H (as prepared in Example 1).

Crystals of ICE in complex with the tetrapeptide aldehyde inhibitor, Ac-Tyr-Val-**Pro**-Asp-H ("**Pro**") were grown under conditions identical to those for crystals of ICE in complex with the tetrapeptide aldehyde inhibitor, Ac-Tyr-Val-**Ala**-Asp-H ("**Ala**").

X-ray diffraction data to 2.8Å resolution was collected on the ICE/**Pro** co-complex. A difference electron density map that combined diffraction data of the form $| F_{Pro} - F_{Ala} |$ and phases calculated from the refined model of the **Ala** inhibited enzyme was used to locate structure changes that had occurred in the ICE/**Pro** co-complex.

Negative features were found in the map wherever localized atoms in the **Ala** complex were removed or shifted by switching to the new ligand. Positive features were found when localized atoms were introduced into the structure, and indicated the new positions of shifted atoms.

Replacement of the alanine that sits in the P2 binding pocket in **Ala** with proline in **Pro** introduced two methylene groups into the structure of the ICE co-complex. The location of these new atoms was indicated by the presence of positive difference electron density adjacent to the beta-carbon of the alanine in the binding pocket P2. Another positive peak nearby indicated the binding of a new water molecule in the **Pro** complex relative to the **Ala** complex. There were also pairs of positive and negative peaks near the tyrosine moiety that sits in the P4 binding pocket of the inhibitor. These peaks indicated shifts in the position of these atoms in the **Pro** complex relative to their location in the **Ala** complex.

These shifts, plus the new atoms referred to above, were modeled, and the resulting structure was refined against the X-ray data to determine a final

picture of the co-complex of Pro with ICE. The space group ($P4_32_12$) and unit cell dimensions (a=b=65 ± 5Å c=162 ± 5Å) for the Pro complex were the same as those observed for the Ala complex.

The ICE structure coordinates known for the first time by virtue of this invention may be used to solve the unknown structure of any mutant, homologue or co-complex of ICE using the above-described method. This method may also be used to determine the binding or orientation of a ligand or chemical entity in the active site or accessory binding site of ICE.

While we have described a number of embodiments of this invention, it is apparent that our basic examples may be altered to provide other embodiments which utilize the products and processes of this invention. Therefore, it will be appreciated that the scope of this invention is to be defined by the appended claims rather than by the specific embodiments which have been represented by way of example.

Tables A and B, following this page, list respectively, the tetramer interface contacts and the structure coordinates of the ICE molecule of this invention.

TABLE A

TETRAMER INTERFACE CONTACTS

Residue		Residue		Residue	
P20	P10	P10	P10	P20	P20
150	375	320	382	240	259
151	371	320	380	267	293
151	372	322	377	268	293
151	375	322	378	274	295
291	323	322	380		
291	321	322	384		
291	322	322	385		
291	323	322	386		
292	321	323	327		
293	321	324	334		
293	319	324	386		
293	320	325	378		
294	318	325	386		
294	319	334	393		
294	320	335	391		
295	318	367	367		
295	319	367	374		
295	320	371	394		
295	321	371	395		
296	317	371	396		
297	317	374	392		
		374	393		
		374	394		
		375	395		
		375	396		
		378	395		
		378	396		
		386	393		
		386	395		
		388	392		
		388	391		
		388	393		
		389	392		
		389	391		
		390	391		

TABLE B

STRUCTURE COORDINATES OF ICE

		Atom Type	RESIDUE	#	X	Y	Z	OCC	B
ATOM	1	C	GLY	131	49.848	81.525	-9.909	1.00	66.26
ATOM	2	O	GLY	131	50.205	82.686	-9.789	1.00	67.80
ATOM	3	HT1	GLY	131	51.316	82.385	-11.694	1.00	0.00
ATOM	4	HT2	GLY	131	49.746	82.510	-12.180	1.00	0.00
ATOM	5	N	GLY	131	50.546	81.841	-12.148	1.00	71.76
ATOM	6	HT3	GLY	131	50.783	81.456	-13.079	1.00	0.00
ATOM	7	CA	GLY	131	50.192	80.805	-11.207	1.00	65.90
ATOM	8	N	ASN	132	49.175	80.916	-8.934	1.00	63.34
ATOM	9	H	ASN	132	48.640	80.121	-9.141	1.00	0.00
ATOM	10	CA	ASN	132	49.178	81.466	-7.566	1.00	57.35
ATOM	11	CB	ASN	132	47.778	81.260	-6.979	1.00	63.76
ATOM	12	CG	ASN	132	47.550	82.132	-5.758	1.00	65.77
ATOM	13	OD1	ASN	132	48.228	83.107	-5.487	1.00	65.21
ATOM	14	ND2	ASN	132	46.506	81.860	-4.997	1.00	67.11
ATOM	15	HD21	ASN	132	45.919	81.109	-5.228	1.00	0.00
ATOM	16	HD22	ASN	132	46.382	82.450	-4.223	1.00	0.00
ATOM	17	C	ASN	132	50.261	80.777	-6.706	1.00	51.45
ATOM	18	O	ASN	132	50.487	80.946	-5.521	1.00	46.19
ATOM	19	N	VAL	133	50.972	79.911	-7.425	1.00	47.07
ATOM	20	H	VAL	133	50.765	79.856	-8.373	1.00	0.00
ATOM	21	CA	VAL	133	52.081	79.094	-6.973	1.00	42.45
ATOM	22	CB	VAL	133	52.214	77.891	-7.947	1.00	39.63
ATOM	23	CG1	VAL	133	53.342	76.953	-7.538	1.00	39.92
ATOM	24	CG2	VAL	133	50.868	77.172	-8.010	1.00	35.70
ATOM	25	C	VAL	133	53.302	79.986	-7.029	1.00	42.39
ATOM	26	O	VAL	133	53.511	80.670	-8.020	1.00	41.5
ATOM	27	N	LYS	134	54.119	79.997	-5.986	1.00	43.94
ATOM	28	NZ	LYS	134	53.921	79.394	-5.236	1.00	0.00
ATOM	29	CA	LYS	134	55.301	80.832	-5.918	1.00	43.48
ATOM	30	CB	LYS	134	55.842	80.694	-4.498	1.00	47.92
ATOM	31	CG	LYS	134	57.200	81.347	-4.244	1.00	58.49
ATOM	32	CD	LYS	134	57.671	81.322	-2.773	1.00	68.37
ATOM	33	CE	LYS	134	56.793	82.161	-1.815	1.00	73.02
ATOM	34	NZ	LYS	134	57.422	82.316	-0.513	1.00	74.14
ATOM	35	HZ1	LYS	134	58.339	82.793	-0.625	1.00	0.00
ATOM	36	HZ2	LYS	134	57.568	81.376	-0.092	1.00	0.00
ATOM	37	HZ3	LYS	134	56.805	82.880	0.105	1.00	0.00
ATOM	38	C	LYS	134	56.311	80.428	-6.979	1.00	43.98
ATOM	39	O	LYS	134	56.604	79.261	-7.186	1.00	40.75
ATOM	40	N	LEU	135	56.897	81.384	-7.698	1.00	45.99
ATOM	41	H	LEU	135	56.807	82.326	-7.445	1.00	0.00
ATOM	42	CA	LEU	135	57.679	81.019	-8.861	1.00	47.05
ATOM	43	CB	LEU	135	57.569	82.064	-9.970	1.00	47.39
ATOM	44	CG	LEU	135	56.156	82.207	-10.535	1.00	45.83
ATOM	45	CD1	LEU	135	56.210	83.182	-11.700	1.00	50.59
ATOM	46	CD2	LEU	135	55.609	80.873	-11.014	1.00	48.32
ATOM	47	C	LEU	135	59.140	80.819	-8.610	1.00	49.94
ATOM	48	O	LEU	135	59.802	81.521	-7.860	1.00	47.32
ATOM	49	N	CYS	136	59.601	79.787	-9.312	1.00	53.47
ATOM	50	H	CYS	136	58.954	79.191	-9.740	1.00	0.00
ATOM	51	CA	CYS	136	61.014	79.522	-9.495	1.00	57.62
ATOM	52	C	CYS	136	61.688	80.552	-10.387	1.00	60.29
ATOM	53	O	CYS	136	61.471	80.621	-11.594	1.00	62.12
ATOM	54	CB	CYS	136	61.208	78.144	-10.115	1.00	53.99
ATOM	55	SG	CYS	136	61.894	76.980	-8.918	1.00	58.70

ATOM	56	N	SER	137	62.538	81.402	-9.833	1.00	59.84
ATOM	57	H	SER	137	62.572	81.519	-8.858	1.00	0.00
ATOM	58	CA	SER	137	63.390	82.210	-10.667	1.00	62.00
ATOM	59	CB	SER	137	64.149	83.158	-9.766	1.00	65.68
ATOM	60	OG	SER	137	63.234	83.655	-8.792	1.00	75.16
ATOM	61	HG	SER	137	62.492	84.111	-9.205	1.00	0.00
ATOM	62	C	SER	137	64.313	81.329	-11.458	1.00	61.26
ATOM	63	O	SER	137	64.602	80.202	-11.086	1.00	62.99
ATOM	64	N	LEU	138	64.823	81.792	-12.585	1.00	61.53
ATOM	65	H	LEU	138	64.686	82.728	-12.829	1.00	0.00
ATOM	66	CA	LEU	138	65.553	80.911	-13.478	1.00	64.28
ATOM	67	CB	LEU	138	65.884	81.695	-14.748	1.00	63.19
ATOM	68	CG	LEU	138	66.536	80.878	-15.866	1.00	61.50
ATOM	69	CD1	LEU	138	65.823	79.540	-16.097	1.00	62.16
ATOM	70	CD2	LEU	138	66.528	81.749	-17.112	1.00	65.07
ATOM	71	C	LEU	138	66.813	80.309	-12.877	1.00	67.11
ATOM	72	O	LEU	138	67.183	79.164	-13.115	1.00	66.56
ATOM	73	N	GLU	139	67.503	81.099	-12.063	1.00	68.85
ATOM	74	H	GLU	139	67.248	82.038	-11.982	1.00	0.00
ATOM	75	CA	GLU	139	68.645	80.591	-11.330	1.00	71.48
ATOM	76	CB	GLU	139	69.271	81.757	-10.558	1.00	78.29
ATOM	77	CG	GLU	139	68.277	82.677	-9.821	1.00	89.52
ATOM	78	CD	GLU	139	68.983	83.966	-9.426	1.00	98.5
ATOM	79	OE1	GLU	139	68.705	85.009	-10.033	1.00	99.9
ATOM	80	OE2	GLU	139	69.811	83.927	-8.510	1.00	101.79
ATOM	81	C	GLU	139	68.241	79.453	-10.411	1.00	69.73
ATOM	82	O	GLU	139	68.938	78.458	-10.328	1.00	70.27
ATOM	83	N	GLU	140	67.107	79.556	-9.711	1.00	67.40
ATOM	84	H	GLU	140	66.567	80.364	-9.814	1.00	0.00
ATOM	85	CA	GLU	140	66.616	78.489	-8.849	1.00	66.30
ATOM	86	CB	GLU	140	65.290	78.874	-8.234	1.00	69.93
ATOM	87	CG	GLU	140	65.411	80.248	-7.577	1.00	79.22
ATOM	88	CD	GLU	140	64.097	80.745	-7.015	1.00	83.51
ATOM	89	OE1	GLU	140	63.207	79.947	-6.716	1.00	86.55
ATOM	90	OE2	GLU	140	63.971	81.956	-6.866	1.00	89.13
ATOM	91	C	GLU	140	66.431	77.221	-9.621	1.00	64.12
ATOM	92	O	GLU	140	66.927	76.166	-9.273	1.00	61.28
ATOM	93	N	ALA	141	65.703	77.298	-10.720	1.00	64.66
ATOM	94	H	ALA	141	65.236	78.135	-10.921	1.00	0.00
ATOM	95	CA	ALA	141	65.611	76.153	-11.604	1.00	68.98
ATOM	96	CB	ALA	141	64.889	76.570	-12.884	1.00	70.25
ATOM	97	C	ALA	141	66.979	75.596	-11.947	1.00	71.14
ATOM	98	O	ALA	141	67.313	74.428	-11.765	1.00	72.56
ATOM	99	N	GLN	142	67.818	76.487	-12.459	1.00	72.92
ATOM	100	OH	GLN	142	67.532	77.424	-12.537	1.00	0.00
ATOM	101	CA	GLN	142	69.151	76.115	-12.892	1.00	73.96
ATOM	102	CB	GLN	142	69.866	77.409	-13.316	1.00	77.97
ATOM	103	CG	GLN	142	70.887	77.279	-14.452	1.00	87.44
ATOM	104	CD	GLN	142	70.264	76.716	-15.714	1.00	92.53
ATOM	105	OE1	GLN	142	70.722	75.733	-16.286	1.00	95.95
ATOM	106	NE2	GLN	142	69.200	77.287	-16.242	1.00	93.80
ATOM	107	HE21	GLN	142	68.816	78.075	-15.810	1.00	0.00
ATOM	108	HE22	GLN	142	68.852	76.862	-17.056	1.00	0.00
ATOM	109	C	GLN	142	69.900	75.373	-11.802	1.00	71.44
ATOM	110	O	GLN	142	70.472	74.312	-12.010	1.00	69.41
ATOM	111	N	ARG	143	69.911	75.911	-10.590	1.00	70.71
ATOM	112	H	ARG	143	69.467	76.774	-10.440	1.00	0.00
ATOM	113	CA	ARG	143	70.560	75.235	-9.482	1.00	71.58
ATOM	114	CB	ARG	143	70.398	76.011	-8.169	1.00	66.09
ATOM	115	CG	ARG	143	71.452	77.103	-8.009	1.00	68.24
ATOM	116	CD	ARG	143	71.260	77.893	-6.715	1.00	67.96
ATOM	117	NE	ARG	143	70.068	78.720	-6.772	1.00	68.10
ATOM	118	HE	ARG	143	69.189	78.300	-6.871	1.00	0.00
ATOM	119	CZ	ARG	143	70.158	80.048	-6.694	1.00	68.46

ATOM	120	NH1	ARG	143	69.028	80.800	-6.754	1.00	68.32
ATOM	121	HH11	ARG	143	68.137	80.358	-6.858	1.00	0.00
ATOM	122	HH12	ARG	143	69.090	81.797	-6.697	1.00	0.00
ATOM	123	NH2	ARG	143	71.365	80.664	-6.550	1.00	68.45
ATOM	124	HH21	ARG	143	72.206	80.125	-6.498	1.00	0.00
ATOM	125	HH22	ARG	143	71.412	81.661	-6.490	1.00	0.00
ATOM	126	C	ARG	143	70.013	73.850	-9.263	1.00	73.97
ATOM	127	O	ARG	143	70.765	72.907	-9.074	1.00	77.08
ATOM	128	N	ILE	144	68.696	73.662	-9.285	1.00	73.91
ATOM	129	H	ILE	144	68.105	74.411	-9.519	1.00	0.00
ATOM	130	CA	ILE	144	68.143	72.352	-8.995	1.00	71.75
ATOM	131	CB	ILE	144	66.605	72.394	-8.986	1.00	69.05
ATOM	132	CG2	ILE	144	66.077	70.990	-8.729	1.00	69.68
ATOM	133	CG1	ILE	144	66.084	73.314	-7.895	1.00	65.22
ATOM	134	CD1	ILE	144	64.588	73.540	-8.061	1.00	62.44
ATOM	135	C	ILE	144	68.604	71.367	-10.036	1.00	72.66
ATOM	136	O	ILE	144	69.045	70.260	-9.743	1.00	71.17
ATOM	137	N	TRP	145	68.507	71.765	-11.304	1.00	75.70
ATOM	138	H	TRP	145	68.167	72.662	-11.514	1.00	0.00
ATOM	139	CA	TRP	145	68.929	70.861	-12.351	1.00	83.94
ATOM	140	CB	TRP	145	68.658	71.462	-13.746	1.00	86.15
ATOM	141	CG	TRP	145	69.038	70.460	-14.839	1.00	93.70
ATOM	142	CD2	TRP	145	68.217	69.255	-15.098	1.00	95.01
ATOM	143	CE2	TRP	145	69.056	68.711	-16.236	1.00	96.30
ATOM	144	CE3	TRP	145	67.071	68.594	-14.711	1.00	94.15
ATOM	145	CD1	TRP	145	70.133	70.564	-15.670	1.00	95.29
ATOM	146	NE1	TRP	145	70.111	69.520	-16.475	1.00	93.47
ATOM	147	HE1	TRP	145	70.787	69.359	-17.166	1.00	0.00
ATOM	148	CZ2	TRP	145	68.642	67.562	-16.873	1.00	100.90
ATOM	149	CZ3	TRP	145	66.717	67.444	-15.394	1.00	96.37
ATOM	150	CH2	TRP	145	67.473	66.945	-16.445	1.00	98.93
ATOM	151	C	TRP	145	70.411	70.588	-12.184	1.00	87.50
ATOM	152	O	TRP	145	70.817	69.442	-12.042	1.00	88.19
ATOM	153	N	ALA	146	71.240	71.638	-12.196	1.00	90.23
ATOM	154	H	ALA	146	70.872	72.546	-12.279	1.00	0.00
ATOM	155	CA	ALA	146	72.678	71.479	-12.055	1.00	90.96
ATOM	156	CB	ALA	146	73.316	72.866	-12.003	1.00	89.47
ATOM	157	C	ALA	146	73.078	70.678	-10.827	1.00	92.53
ATOM	158	O	ALA	146	74.075	69.975	-10.833	1.00	93.84
ATOM	159	N	GLN	147	72.310	70.767	-9.739	1.00	93.24
ATOM	160	H	GLN	147	71.578	71.421	-9.711	1.00	0.00
ATOM	161	CA	GLN	147	72.543	69.925	-8.583	1.00	94.09
ATOM	162	CB	GLN	147	71.690	70.379	-7.387	1.00	96.74
ATOM	163	CG	GLN	147	72.033	69.642	-6.090	1.00	102.36
ATOM	164	CD	GLN	147	70.829	69.585	-5.181	1.00	107.75
ATOM	165	OE1	GLN	147	69.729	70.018	-5.491	1.00	109.80
ATOM	166	NE2	GLN	147	70.957	68.991	-4.006	1.00	109.34
ATOM	167	HE21	GLN	147	71.821	68.602	-3.760	1.00	0.00
ATOM	168	HE22	GLN	147	70.155	68.987	-3.438	1.00	0.00
ATOM	169	C	GLN	147	72.216	68.479	-8.875	1.00	93.64
ATOM	170	O	GLN	147	73.058	67.595	-8.801	1.00	93.43
ATOM	171	N	LYS	148	70.969	68.171	-9.211	1.00	91.82
ATOM	172	H	LYS	148	70.319	68.869	-9.439	1.00	0.00
ATOM	173	CA	LYS	148	70.621	66.770	-9.239	1.00	89.79
ATOM	174	CB	LYS	148	69.339	66.539	-8.438	1.00	91.49
ATOM	175	CG	LYS	148	69.449	66.861	-6.954	1.00	91.59
ATOM	176	CD	LYS	148	68.211	66.386	-6.193	1.00	94.76
ATOM	177	CE	LYS	148	68.288	66.715	-4.706	1.00	97.17
ATOM	178	NZ	LYS	148	69.521	66.190	-4.145	1.00	102.16
ATOM	179	HZ1	LYS	148	70.339	66.615	-4.627	1.00	0.00
ATOM	180	HZ2	LYS	148	69.553	65.158	-4.275	1.00	0.00
ATOM	181	HZ3	LYS	148	69.574	66.411	-3.131	1.00	0.00
ATOM	182	C	LYS	148	70.457	66.096	-10.578	1.00	87.23
ATOM	183	O	LYS	148	70.294	64.882	-10.625	1.00	88.22

ATOM	184	N	ALA	149	70.496	66.825	-11.691	1.00	83.64
ATOM	185	H	ALA	149	70.728	67.775	-11.599	1.00	0.00
ATOM	186	CA	ALA	149	70.271	66.316	-13.039	1.00	81.28
ATOM	187	CB	ALA	149	71.416	66.848	-13.906	1.00	80.46
ATOM	188	C	ALA	149	70.092	64.807	-13.272	1.00	80.23
ATOM	189	O	ALA	149	69.034	64.377	-13.709	1.00	81.20
ATOM	190	N	ALA	150	71.079	63.939	-13.002	1.00	77.26
ATOM	191	H	ALA	150	71.903	64.290	-12.604	1.00	0.00
ATOM	192	CA	ALA	150	70.928	62.493	-13.224	1.00	72.54
ATOM	193	CB	ALA	150	72.254	61.803	-12.872	1.00	71.93
ATOM	194	C	ALA	150	69.786	61.803	-12.458	1.00	67.17
ATOM	195	O	ALA	150	69.332	60.728	-12.832	1.00	64.24
ATOM	196	N	GLU	151	69.298	62.391	-11.366	1.00	58.90
ATOM	197	H	GLU	151	69.693	63.225	-11.031	1.00	0.00
ATOM	198	CA	GLU	151	68.153	61.823	-10.700	1.00	55.46
ATOM	199	CB	GLU	151	68.612	61.333	-9.316	1.00	60.03
ATOM	200	CG	GLU	151	69.510	60.091	-9.532	1.00	67.91
ATOM	201	CD	GLU	151	69.733	59.292	-8.259	1.00	72.08
ATOM	202	OE1	GLU	151	68.753	58.778	-7.702	1.00	75.94
ATOM	203	OE2	GLU	151	70.887	59.159	-7.846	1.00	70.44
ATOM	204	C	GLU	151	66.966	62.759	-10.610	1.00	49.03
ATOM	205	O	GLU	151	66.237	62.811	-9.632	1.00	40.75
ATOM	206	N	ILE	152	66.751	63.538	-11.671	1.00	46.24
ATOM	207	H	ILE	152	67.390	63.525	-12.419	1.00	0.00
ATOM	208	CA	ILE	152	65.578	64.379	-11.820	1.00	41.23
ATOM	209	CB	ILE	152	66.006	65.876	-11.979	1.00	41.97
ATOM	210	CG2	ILE	152	64.846	66.776	-12.375	1.00	37.44
ATOM	211	CG1	ILE	152	66.456	66.419	-10.633	1.00	39.50
ATOM	212	CD1	ILE	152	67.026	67.826	-10.790	1.00	45.38
ATOM	213	C	ILE	152	64.838	63.880	-13.063	1.00	39.41
ATOM	214	O	ILE	152	65.399	63.521	-14.089	1.00	38.70
ATOM	215	N	TYR	153	63.506	63.846	-12.966	1.00	37.18
ATOM	216	H	TYR	153	63.125	64.015	-12.080	1.00	0.00
ATOM	217	CA	TYR	153	62.606	63.601	-14.098	1.00	34.02
ATOM	218	CB	TYR	153	61.131	63.521	-13.608	1.00	30.99
ATOM	219	CG	TYR	153	60.815	62.157	-13.006	1.00	28.21
ATOM	220	CD1	TYR	153	60.889	61.023	-13.795	1.00	27.24
ATOM	221	CE1	TYR	153	60.661	59.769	-13.266	1.00	25.65
ATOM	222	CD2	TYR	153	60.496	62.024	-11.663	1.00	24.92
ATOM	223	CE2	TYR	153	60.266	60.774	-11.126	1.00	20.91
ATOM	224	CZ	TYR	153	60.352	59.657	-11.934	1.00	24.92
ATOM	225	OH	TYR	153	60.116	58.405	-11.404	1.00	22.74
ATOM	226	HH	TYR	153	59.896	58.542	-10.481	1.00	0.00
ATOM	227	C	TYR	153	62.734	64.754	-15.092	1.00	31.41
ATOM	228	O	TYR	153	62.545	65.895	-14.708	1.00	30.52
ATOM	229	N	PRO	154	63.045	64.585	-16.332	1.00	29.09
ATOM	230	CD	PRO	154	63.433	63.298	-16.886	1.00	26.14
ATOM	231	CA	PRO	154	63.119	65.685	-17.300	1.00	26.59
ATOM	232	CB	PRO	154	63.791	65.078	-18.508	1.00	21.73
ATOM	233	CG	PRO	154	63.408	63.614	-18.383	1.00	26.66
ATOM	234	C	PRO	154	61.782	66.309	-17.627	1.00	27.17
ATOM	235	O	PRO	154	60.763	65.693	-17.860	1.00	30.28
ATOM	236	N	ILE	155	61.791	67.620	-17.645	1.00	27.49
ATOM	237	H	ILE	155	62.636	68.068	-17.453	1.00	0.00
ATOM	238	CA	ILE	155	60.623	68.417	-17.912	1.00	27.05
ATOM	239	CB	ILE	155	60.810	69.687	-17.067	1.00	27.13
ATOM	240	CG2	ILE	155	59.893	70.851	-17.429	1.00	28.62
ATOM	241	CG1	ILE	155	60.584	69.235	-15.624	1.00	27.98
ATOM	242	CD1	ILE	155	59.370	68.340	-15.354	1.00	30.26
ATOM	243	C	ILE	155	60.648	68.636	-19.414	1.00	33.41
ATOM	244	O	ILE	155	61.715	68.804	-19.990	1.00	34.72
ATOM	245	N	MET	156	59.510	68.638	-20.116	1.00	33.95
ATOM	246	H	MET	156	58.677	68.455	-19.642	1.00	0.00
ATOM	247	CA	MET	156	59.471	68.939	-21.542	1.00	31.70

ATOM	248	CB	MET	156	58.252	68.339	-22.224	1.00	31.01
ATOM	249	CG	MET	156	58.574	67.001	-22.838	1.00	30.35
ATOM	250	SD	MET	156	57.118	66.252	-23.577	1.00	39.82
ATOM	251	CE	MET	156	57.590	64.545	-23.528	1.00	34.89
ATOM	252	C	MET	156	59.384	70.434	-21.735	1.00	34.78
ATOM	253	O	MET	156	59.035	71.208	-20.854	1.00	32.33
ATOM	254	N	ASP	157	59.711	70.869	-22.942	1.00	37.95
ATOM	255	H	ASP	157	59.923	70.224	-23.648	1.00	0.00
ATOM	256	CA	ASP	157	59.715	72.281	-23.240	1.00	38.36
ATOM	257	CB	ASP	157	60.385	72.438	-24.613	1.00	51.68
ATOM	258	CG	ASP	157	60.369	73.848	-25.178	1.00	61.42
ATOM	259	OD1	ASP	157	60.483	73.957	-26.401	1.00	68.30
ATOM	260	OD2	ASP	157	60.249	74.822	-24.421	1.00	67.14
ATOM	261	C	ASP	157	58.315	72.829	-23.203	1.00	31.15
ATOM	262	O	ASP	157	57.360	72.284	-23.730	1.00	27.50
ATOM	263	N	LYS	158	58.232	73.965	-22.543	1.00	30.63
ATOM	264	H	LYS	158	59.032	74.318	-22.102	1.00	0.00
ATOM	265	CA	LYS	158	56.975	74.638	-22.320	1.00	33.69
ATOM	266	CB	LYS	158	57.265	75.906	-21.540	1.00	34.01
ATOM	267	CG	LYS	158	56.037	76.664	-21.085	1.00	40.80
ATOM	268	CD	LYS	158	56.390	77.826	-20.154	1.00	48.58
ATOM	269	CE	LYS	158	55.152	78.472	-19.524	1.00	52.61
ATOM	270	NZ	LYS	158	55.537	79.342	-18.431	1.00	59.47
ATOM	271	HZ1	LYS	158	56.154	80.095	-18.794	1.00	0.00
ATOM	272	HZ2	LYS	158	56.050	78.792	-17.712	1.00	0.00
ATOM	273	HZ3	LYS	158	54.691	79.763	-17.998	1.00	0.00
ATOM	274	C	LYS	158	56.275	74.942	-23.618	1.00	38.44
ATOM	275	O	LYS	158	55.076	74.803	-23.735	1.00	41.75
ATOM	276	N	SER	159	56.962	75.367	-24.672	1.00	41.20
ATOM	277	H	SER	159	57.938	75.470	-24.645	1.00	0.00
ATOM	278	CA	SER	159	56.297	75.717	-25.916	1.00	39.99
ATOM	279	CB	SER	159	57.304	76.202	-26.930	1.00	39.69
ATOM	280	OG	SER	159	58.553	75.552	-26.729	1.00	40.47
ATOM	281	HG	SER	159	58.453	74.606	-26.880	1.00	0.00
ATOM	282	C	SER	159	55.543	74.590	-26.548	1.00	40.83
ATOM	283	O	SER	159	54.666	74.774	-27.370	1.00	43.09
ATOM	284	N	SER	160	55.886	73.373	-26.184	1.00	43.73
ATOM	285	H	SER	160	56.444	73.181	-25.399	1.00	0.00
ATOM	286	CA	SER	160	55.410	72.261	-26.959	1.00	45.71
ATOM	287	CB	SER	160	56.592	71.756	-27.769	1.00	45.15
ATOM	288	OG	SER	160	57.835	71.958	-27.083	1.00	53.30
ATOM	289	HG	SER	160	58.517	71.533	-27.614	1.00	0.00
ATOM	290	C	SER	160	54.800	71.154	-26.121	1.00	45.78
ATOM	291	O	SER	160	54.262	70.217	-26.700	1.00	48.03
ATOM	292	N	ARG	161	54.842	71.162	-24.782	1.00	38.45
ATOM	293	H	ARG	161	55.201	71.921	-24.278	1.00	0.00
ATOM	294	CA	ARG	161	54.322	70.004	-24.097	1.00	32.89
ATOM	295	CB	ARG	161	54.987	69.929	-22.727	1.00	31.71
ATOM	296	CG	ARG	161	54.631	71.054	-21.769	1.00	29.23
ATOM	297	CD	ARG	161	55.579	71.078	-20.571	1.00	26.52
ATOM	298	NE	ARG	161	55.148	72.182	-19.760	1.00	23.86
ATOM	299	HE	ARG	161	54.189	72.357	-19.663	1.00	0.00
ATOM	300	CZ	ARG	161	56.001	72.971	-19.138	1.00	24.88
ATOM	301	NH1	ARG	161	55.486	74.036	-18.477	1.00	23.22
ATOM	302	HH11	ARG	161	54.499	74.198	-18.481	1.00	0.00
ATOM	303	HH12	ARG	161	56.093	74.673	-18.006	1.00	0.00
ATOM	304	NH2	ARG	161	57.339	72.712	-19.115	1.00	26.60
ATOM	305	HH21	ARG	161	57.703	71.901	-19.572	1.00	0.00
ATOM	306	HH22	ARG	161	57.957	73.331	-18.630	1.00	0.00
ATOM	307	C	ARG	161	52.816	70.077	-23.999	1.00	30.40
ATOM	308	O	ARG	161	52.219	71.144	-23.981	1.00	30.63
ATOM	309	N	THR	162	52.134	68.955	-23.937	1.00	25.20
ATOM	310	H	THR	162	52.595	68.099	-24.073	1.00	0.00
ATOM	311	CA	THR	162	50.699	68.963	-23.791	1.00	23.14

ATOM	312	CB	THR	162	50.068	68.276	-25.028	1.00	23.65
ATOM	313	OG1	THR	162	50.780	67.056	-25.252	1.00	26.56
ATOM	314	HG1	THR	162	50.721	66.510	-24.445	1.00	0.00
ATOM	315	CG2	THR	162	50.148	69.114	-26.306	1.00	23.19
ATOM	316	C	THR	162	50.373	68.219	-22.510	1.00	25.37
ATOM	317	O	THR	162	50.062	67.030	-22.548	1.00	27.75
ATOM	318	N	ARG	163	50.423	68.826	-21.340	1.00	24.62
ATOM	319	H	ARG	163	50.560	69.797	-21.312	1.00	0.00
ATOM	320	CA	ARG	163	50.174	68.133	-20.077	1.00	24.12
ATOM	321	CB	ARG	163	50.757	68.905	-18.918	1.00	15.48
ATOM	322	CG	ARG	163	52.227	68.612	-18.793	1.00	17.34
ATOM	323	CD	ARG	163	52.721	69.593	-17.772	1.00	18.83
ATOM	324	NE	ARG	163	54.136	69.427	-17.669	1.00	24.11
ATOM	325	HE	ARG	163	54.592	68.736	-18.195	1.00	0.00
ATOM	326	CZ	ARG	163	54.822	70.232	-16.883	1.00	25.67
ATOM	327	NH1	ARG	163	56.160	70.051	-16.807	1.00	34.46
ATOM	328	HH11	ARG	163	56.596	69.318	-17.328	1.00	0.00
ATOM	329	HH12	ARG	163	56.710	70.634	-16.209	1.00	0.00
ATOM	330	NH2	ARG	163	54.219	71.220	-16.167	1.00	27.39
ATOM	331	HH21	ARG	163	53.229	71.357	-16.223	1.00	0.00
ATOM	332	HH22	ARG	163	54.772	71.806	-15.575	1.00	0.00
ATOM	333	C	ARG	163	48.738	67.876	-19.714	1.00	24.62
ATOM	334	O	ARG	163	47.893	68.762	-19.750	1.00	29.04
ATOM	335	N	LEU	164	48.357	66.667	-19.340	1.00	23.75
ATOM	336	H	LEU	164	49.023	65.971	-19.147	1.00	0.00
ATOM	337	CA	LEU	164	46.944	66.455	-19.043	1.00	24.57
ATOM	338	CB	LEU	164	46.366	65.336	-19.893	1.00	27.72
ATOM	339	CG	LEU	164	45.556	65.607	-21.165	1.00	28.04
ATOM	340	CD1	LEU	164	46.108	66.789	-21.926	1.00	30.94
ATOM	341	CD2	LEU	164	45.573	64.331	-22.006	1.00	27.16
ATOM	342	C	LEU	164	46.774	66.047	-17.612	1.00	23.76
ATOM	343	O	LEU	164	47.607	65.281	-17.142	1.00	22.71
ATOM	344	N	ALA	165	45.733	66.505	-16.907	1.00	21.51
ATOM	345	H	ALA	165	45.124	67.175	-17.292	1.00	0.00
ATOM	346	CA	ALA	165	45.396	65.986	-15.589	1.00	24.14
ATOM	347	CB	ALA	165	45.687	67.006	-14.488	1.00	21.16
ATOM	348	C	ALA	165	43.924	65.668	-15.543	1.00	24.40
ATOM	349	O	ALA	165	43.162	66.279	-16.279	1.00	25.81
ATOM	350	N	LEU	166	43.495	64.730	-14.699	1.00	24.86
ATOM	351	H	LEU	166	44.143	64.282	-14.114	1.00	0.00
ATOM	352	CA	LEU	166	42.091	64.361	-14.592	1.00	27.92
ATOM	353	CB	LEU	166	41.914	62.948	-15.196	1.00	23.03
ATOM	354	CG	LEU	166	40.571	62.280	-14.919	1.00	20.45
ATOM	355	CD1	LEU	166	39.446	62.990	-15.658	1.00	14.43
ATOM	356	CD2	LEU	166	40.691	60.807	-15.320	1.00	21.71
ATOM	357	C	LEU	166	41.580	64.404	-13.149	1.00	28.64
ATOM	358	O	LEU	166	42.207	63.838	-12.261	1.00	26.66
ATOM	359	N	ILE	167	40.441	65.079	-12.901	1.00	27.07
ATOM	360	H	ILE	167	39.991	65.549	-13.638	1.00	0.00
ATOM	361	CA	ILE	167	39.802	65.137	-11.600	1.00	21.18
ATOM	362	CB	ILE	167	39.494	66.602	-11.205	1.00	20.90
ATOM	363	CG2	ILE	167	38.719	66.663	-9.893	1.00	21.77
ATOM	364	CG1	ILE	167	40.793	67.354	-11.003	1.00	17.47
ATOM	365	CD1	ILE	167	40.499	68.753	-10.522	1.00	17.98
ATOM	366	C	ILE	167	38.513	64.358	-11.684	1.00	24.82
ATOM	367	O	ILE	167	37.634	64.653	-12.493	1.00	23.12
ATOM	368	N	ILE	168	38.333	63.328	-10.865	1.00	25.26
ATOM	369	H	ILE	168	39.066	63.004	-10.297	1.00	0.00
ATOM	370	CA	ILE	168	37.022	62.731	-10.757	1.00	23.44
ATOM	371	CB	ILE	168	37.119	61.228	-11.076	1.00	23.97
ATOM	372	CG2	ILE	168	35.741	60.582	-10.863	1.00	28.80
ATOM	373	CG1	ILE	168	37.581	61.030	-12.546	1.00	22.39
ATOM	374	CD1	ILE	168	37.869	59.587	-12.959	1.00	22.21
ATOM	375	C	ILE	168	36.506	62.981	-9.353	1.00	24.34

ATOM	376	O	ILE	168	37.126	62.633	-8.356	1.00	23.09
ATOM	377	N	CYS	169	35.337	63.613	-9.260	1.00	26.60
ATOM	378	H	CYS	169	34.821	63.777	-10.079	1.00	0.00
ATOM	379	CA	CYS	169	34.765	64.030	-7.986	1.00	27.82
ATOM	380	CB	CYS	169	34.847	65.544	-7.831	1.00	26.82
ATOM	381	SG	CYS	169	34.147	66.177	-6.282	1.00	31.50
ATOM	382	C	CYS	169	33.323	63.629	-7.866	1.00	28.36
ATOM	383	O	CYS	169	32.520	63.950	-8.735	1.00	25.83
ATOM	384	N	ASN	170	32.948	62.918	-6.803	1.00	27.23
ATOM	385	H	ASN	170	33.617	62.683	-6.124	1.00	0.00
ATOM	386	CA	ASN	170	31.554	62.555	-6.619	1.00	29.76
ATOM	387	CB	ASN	170	31.372	61.071	-6.286	1.00	26.22
ATOM	388	CG	ASN	170	31.674	60.138	-7.440	1.00	29.16
ATOM	389	OD1	ASN	170	31.709	60.485	-8.614	1.00	32.47
ATOM	390	ND2	ASN	170	31.970	58.887	-7.151	1.00	25.45
ATOM	391	HD21	ASN	170	32.015	58.569	-6.216	1.00	0.00
ATOM	392	HD22	ASN	170	32.132	58.288	-7.901	1.00	0.00
ATOM	393	C	ASN	170	30.957	63.328	-5.478	1.00	32.01
ATOM	394	O	ASN	170	31.382	63.086	-4.361	1.00	34.71
ATOM	395	N	GLU	171	30.000	64.247	-5.672	1.00	36.94
ATOM	396	H	GLU	171	29.711	64.420	-6.594	1.00	0.00
ATOM	397	CA	GLU	171	29.301	64.905	-4.558	1.00	39.76
ATOM	398	CB	GLU	171	29.119	66.413	-4.822	1.00	36.97
ATOM	399	CG	GLU	171	28.418	67.084	-3.634	1.00	43.98
ATOM	400	CD	GLU	171	28.233	68.579	-3.777	1.00	47.95
ATOM	401	OE1	GLU	171	28.302	69.095	-4.890	1.00	53.49
ATOM	402	OE2	GLU	171	28.003	69.233	-2.761	1.00	48.17
ATOM	403	C	GLU	171	27.914	64.338	-4.240	1.00	41.90
ATOM	404	O	GLU	171	27.509	64.214	-3.096	1.00	40.97
ATOM	405	N	GLU	172	27.133	63.976	-5.251	1.00	48.24
ATOM	406	H	GLU	172	27.505	63.929	-6.159	1.00	0.00
ATOM	407	CA	GLU	172	25.760	63.534	-5.050	1.00	51.31
ATOM	408	CB	GLU	172	24.802	64.170	-6.061	1.00	55.01
ATOM	409	CG	GLU	172	23.819	65.134	-5.408	1.00	66.24
ATOM	410	CD	GLU	172	24.170	66.580	-5.699	1.00	74.35
ATOM	411	OE1	GLU	172	23.249	67.402	-5.708	1.00	81.11
ATOM	412	OE2	GLU	172	25.342	66.893	-5.911	1.00	76.04
ATOM	413	C	GLU	172	25.676	62.035	-5.242	1.00	49.78
ATOM	414	O	GLU	172	26.092	61.501	-6.266	1.00	46.42
ATOM	415	N	PHE	173	25.125	61.338	-4.250	1.00	49.39
ATOM	416	H	PHE	173	24.695	61.780	-3.485	1.00	0.00
ATOM	417	CA	PHE	173	25.085	59.888	-4.303	1.00	53.47
ATOM	418	CB	PHE	173	25.878	59.313	-3.142	1.00	50.77
ATOM	419	CG	PHE	173	27.371	59.547	-3.286	1.00	46.81
ATOM	420	CD1	PHE	173	28.173	58.521	-3.768	1.00	40.36
ATOM	421	CD2	PHE	173	27.927	60.747	-2.867	1.00	42.17
ATOM	422	CE1	PHE	173	29.535	58.684	-3.778	1.00	37.00
ATOM	423	CE2	PHE	173	29.291	60.904	-2.902	1.00	38.90
ATOM	424	CZ	PHE	173	30.089	59.870	-3.332	1.00	39.65
ATOM	425	C	PHE	173	23.661	59.372	-4.221	1.00	56.41
ATOM	426	O	PHE	173	22.772	60.010	-3.675	1.00	60.38
ATOM	427	N	ASP	174	23.394	58.194	-4.764	1.00	54.59
ATOM	428	H	ASP	174	24.131	57.657	-5.134	1.00	0.00
ATOM	429	CA	ASP	174	22.044	57.658	-4.745	1.00	53.81
ATOM	430	CB	ASP	174	21.943	56.370	-5.557	1.00	51.10
ATOM	431	CG	ASP	174	22.091	56.666	-7.030	1.00	53.87
ATOM	432	OD1	ASP	174	22.150	55.698	-7.795	1.00	53.10
ATOM	433	OD2	ASP	174	22.148	57.850	-7.408	1.00	53.80
ATOM	434	C	ASP	174	21.500	57.347	-3.370	1.00	56.79
ATOM	435	O	ASP	174	20.317	57.447	-3.086	1.00	60.64
ATOM	436	N	SER	175	22.354	56.940	-2.457	1.00	57.04
ATOM	437	H	SER	175	23.312	57.026	-2.628	1.00	0.00
ATOM	438	CA	SER	175	21.856	56.461	-1.185	1.00	56.82
ATOM	439	CB	SER	175	22.007	54.938	-1.152	1.00	53.73

ATOM	440	OG	SER	175	21.821	54.307	-2.423	1.00	50.93
ATOM	441	HG	SER	175	22.453	54.685	-3.041	1.00	0.00
ATOM	442	C	SER	175	22.614	57.115	-0.038	1.00	59.19
ATOM	443	O	SER	175	22.050	57.584	0.945	1.00	63.80
ATOM	444	N	ILE	176	23.949	57.172	-0.133	1.00	57.13
ATOM	445	H	ILE	176	24.384	56.889	-0.963	1.00	0.00
ATOM	446	CA	ILE	176	24.725	57.758	0.942	1.00	50.84
ATOM	447	CB	ILE	176	26.167	57.155	0.920	1.00	52.16
ATOM	448	CG2	ILE	176	25.982	55.645	1.127	1.00	54.09
ATOM	449	CG1	ILE	176	26.947	57.381	-0.375	1.00	51.82
ATOM	450	CD1	ILE	176	28.205	56.486	-0.451	1.00	47.41
ATOM	451	C	ILE	176	24.716	59.262	0.770	1.00	47.11
ATOM	452	O	ILE	176	24.516	59.755	-0.332	1.00	45.21
ATOM	453	N	PRO	177	24.918	60.009	1.801	1.00	47.09
ATOM	454	CD	PRO	177	25.067	59.502	3.162	1.00	46.36
ATOM	455	CA	PRO	177	24.821	61.475	1.806	1.00	48.52
ATOM	456	CB	PRO	177	24.733	61.862	3.280	1.00	45.72
ATOM	457	CG	PRO	177	25.513	60.744	3.937	1.00	45.89
ATOM	458	C	PRO	177	25.870	62.308	1.096	1.00	51.58
ATOM	459	O	PRO	177	27.078	62.045	1.042	1.00	56.38
ATOM	460	N	ARG	178	25.287	63.373	0.559	1.00	50.95
ATOM	461	H	ARG	178	24.351	63.552	0.778	1.00	0.00
ATOM	462	CA	ARG	178	25.959	64.288	-0.328	1.00	52.24
ATOM	463	CB	ARG	178	24.910	65.270	-0.842	1.00	54.80
ATOM	464	CG	ARG	178	25.505	66.396	-1.661	1.00	62.55
ATOM	465	CD	ARG	178	24.484	67.300	-2.273	1.00	67.32
ATOM	466	NE	ARG	178	25.167	68.507	-2.664	1.00	77.79
ATOM	467	HE	ARG	178	26.144	68.522	-2.727	1.00	0.00
ATOM	468	CZ	ARG	178	24.473	69.607	-2.918	1.00	85.85
ATOM	469	NH1	ARG	178	23.102	69.585	-2.899	1.00	92.67
ATOM	470	HH11	ARG	178	22.609	68.736	-2.708	1.00	0.00
ATOM	471	HH12	ARG	178	22.586	70.415	-3.103	1.00	0.00
ATOM	472	NH2	ARG	178	25.133	70.773	-3.165	1.00	90.17
ATOM	473	HH21	ARG	178	26.133	70.802	-3.145	1.00	0.00
ATOM	474	HH22	ARG	178	24.609	71.605	-3.354	1.00	0.00
ATOM	475	C	ARG	178	27.133	65.020	0.280	1.00	49.82
ATOM	476	O	ARG	178	27.078	65.589	1.354	1.00	51.03
ATOM	477	N	ARG	179	28.243	65.007	-0.439	1.00	47.03
ATOM	478	H	ARG	179	28.218	64.607	-1.336	1.00	0.00
ATOM	479	CA	ARG	179	29.458	65.625	0.039	1.00	42.75
ATOM	480	CB	ARG	179	30.625	64.919	-0.632	1.00	42.27
ATOM	481	CG	ARG	179	30.599	63.395	-0.447	1.00	39.14
ATOM	482	CD	ARG	179	31.739	62.682	-1.159	1.00	40.61
ATOM	483	NE	ARG	179	33.057	63.164	-0.704	1.00	40.03
ATOM	484	HE	ARG	179	33.387	62.869	0.169	1.00	0.00
ATOM	485	CZ	ARG	179	33.827	63.996	-1.427	1.00	40.60
ATOM	486	NH1	ARG	179	33.483	64.391	-2.691	1.00	35.23
ATOM	487	HH11	ARG	179	32.630	64.075	-3.103	1.00	0.00
ATOM	488	HH12	ARG	179	34.077	65.023	-3.191	1.00	0.00
ATOM	489	NH2	ARG	179	34.965	64.483	-0.859	1.00	35.40
ATOM	490	HH21	ARG	179	35.205	64.214	0.074	1.00	0.00
ATOM	491	HH22	ARG	179	35.562	65.100	-1.370	1.00	0.00
ATOM	492	C	ARG	179	29.512	67.124	-0.198	1.00	44.55
ATOM	493	O	ARG	179	30.215	67.684	-1.034	1.00	44.42
ATOM	494	N	THR	180	28.730	67.862	0.570	1.00	45.86
ATOM	495	H	THR	180	28.063	67.420	1.138	1.00	0.00
ATOM	496	CA	THR	180	28.816	69.308	0.548	1.00	46.36
ATOM	497	CB	THR	180	27.770	69.840	1.532	1.00	50.60
ATOM	498	OG1	THR	180	26.517	69.456	0.968	1.00	54.63
ATOM	499	HG1	THR	180	25.800	69.689	1.568	1.00	0.00
ATOM	500	CG2	THR	180	27.792	71.351	1.735	1.00	53.13
ATOM	501	C	THR	180	30.221	69.783	0.901	1.00	46.41
ATOM	502	O	THR	180	30.882	69.285	1.807	1.00	47.93
ATOM	503	N	GLY	181	30.713	70.783	0.171	1.00	46.30

ATOM	504	H	GLY	181	30.090	71.312	-0.350	1.00	0.00
ATOM	505	CA	GLY	181	32.118	71.193	0.236	1.00	41.25
ATOM	506	C	GLY	181	32.915	70.679	-0.948	1.00	40.64
ATOM	507	O	GLY	181	34.005	71.154	-1.278	1.00	37.29
ATOM	508	N	ALA	182	32.381	69.688	-1.672	1.00	35.93
ATOM	509	H	ALA	182	31.540	69.257	-1.418	1.00	0.00
ATOM	510	CA	ALA	182	33.136	69.171	-2.785	1.00	39.67
ATOM	511	CB	ALA	182	32.314	68.028	-3.377	1.00	35.68
ATOM	512	C	ALA	182	33.503	70.220	-3.824	1.00	39.67
ATOM	513	O	ALA	182	34.590	70.239	-4.378	1.00	40.75
ATOM	514	N	GLU	183	32.599	71.153	-4.107	1.00	42.72
ATOM	515	H	GLU	183	31.748	71.149	-3.627	1.00	0.00
ATOM	516	CA	GLU	183	32.824	72.180	-5.108	1.00	40.12
ATOM	517	CB	GLU	183	31.614	73.091	-5.246	1.00	47.30
ATOM	518	CG	GLU	183	31.637	73.914	-6.544	1.00	63.74
ATOM	519	CD	GLU	183	30.918	73.216	-7.697	1.00	71.48
ATOM	520	OE1	GLU	183	30.272	73.920	-8.481	1.00	78.62
ATOM	521	OE2	GLU	183	30.994	71.988	-7.818	1.00	76.00
ATOM	522	C	GLU	183	33.998	73.045	-4.776	1.00	35.44
ATOM	523	O	GLU	183	34.778	73.390	-5.639	1.00	37.02
ATOM	524	N	VAL	184	34.197	73.424	-3.521	1.00	32.69
ATOM	525	H	VAL	184	33.502	73.236	-2.857	1.00	0.00
ATOM	526	CA	VAL	184	35.437	74.093	-3.114	1.00	32.56
ATOM	527	CB	VAL	184	35.391	74.286	-1.598	1.00	30.19
ATOM	528	CG1	VAL	184	36.568	75.090	-1.054	1.00	28.08
ATOM	529	CG2	VAL	184	34.081	74.992	-1.308	1.00	34.05
ATOM	530	C	VAL	184	36.707	73.335	-3.505	1.00	31.95
ATOM	531	O	VAL	184	37.716	73.836	-3.987	1.00	31.94
ATOM	532	N	ASP	185	36.649	72.025	-3.278	1.00	36.44
ATOM	533	H	ASP	185	35.811	71.642	-2.945	1.00	0.00
ATOM	534	CA	ASP	185	37.768	71.151	-3.586	1.00	32.53
ATOM	535	CB	ASP	185	37.470	69.728	-3.077	1.00	33.96
ATOM	536	CG	ASP	185	37.375	69.592	-1.539	1.00	35.35
ATOM	537	OD1	ASP	185	38.047	70.367	-0.833	1.00	28.61
ATOM	538	OD2	ASP	185	36.635	68.705	-1.082	1.00	32.20
ATOM	539	C	ASP	185	38.020	71.139	-5.059	1.00	30.28
ATOM	540	O	ASP	185	39.161	71.233	-5.493	1.00	29.51
ATOM	541	N	ILE	186	36.956	71.032	-5.849	1.00	29.28
ATOM	542	H	ILE	186	36.070	70.902	-5.447	1.00	0.00
ATOM	543	CA	ILE	186	37.096	71.078	-7.305	1.00	31.19
ATOM	544	CB	ILE	186	35.728	70.861	-8.016	1.00	31.31
ATOM	545	CG2	ILE	186	35.874	71.027	-9.544	1.00	29.98
ATOM	546	CG1	ILE	186	35.212	69.446	-7.688	1.00	33.52
ATOM	547	CD1	ILE	186	33.829	69.127	-8.292	1.00	24.25
ATOM	548	C	ILE	186	37.684	72.413	-7.748	1.00	30.16
ATOM	549	O	ILE	186	38.691	72.466	-8.447	1.00	30.56
ATOM	550	N	THR	187	37.132	73.560	-7.388	1.00	27.47
ATOM	551	H	THR	187	36.310	73.583	-6.842	1.00	0.00
ATOM	552	CA	THR	187	37.739	74.820	-7.788	1.00	27.93
ATOM	553	CB	THR	187	36.943	75.985	-7.175	1.00	27.45
ATOM	554	OG1	THR	187	35.600	75.803	-7.625	1.00	32.61
ATOM	555	HG1	THR	187	35.578	75.839	-8.583	1.00	0.00
ATOM	556	CG2	THR	187	37.461	77.371	-7.566	1.00	24.19
ATOM	557	C	THR	187	39.193	74.935	-7.395	1.00	28.16
ATOM	558	O	THR	187	39.997	75.448	-8.163	1.00	28.74
ATOM	559	N	GLY	188	39.561	74.456	-6.203	1.00	28.71
ATOM	560	H	GLY	188	38.908	74.010	-5.619	1.00	0.00
ATOM	561	CA	GLY	188	40.932	74.607	-5.753	1.00	25.69
ATOM	562	C	GLY	188	41.872	73.681	-6.483	1.00	27.48
ATOM	563	O	GLY	188	42.983	74.024	-6.871	1.00	28.61
ATOM	564	N	MET	189	41.491	72.438	-6.720	1.00	27.34
ATOM	565	H	MET	189	40.618	72.115	-6.415	1.00	0.00
ATOM	566	CA	MET	189	42.405	71.582	-7.426	1.00	25.62
ATOM	567	CB	MET	189	42.016	70.117	-7.218	1.00	31.58

ATOM	568	CG	MET	189	42.445	69.542	-5.843	1.00	37.74
ATOM	569	SD	MET	189	44.201	69.754	-5.409	1.00	37.50
ATOM	570	CE	MET	189	44.983	68.533	-6.417	1.00	38.22
ATOM	571	C	MET	189	42.477	71.893	-8.893	1.00	24.18
ATOM	572	O	MET	189	43.559	71.814	-9.460	1.00	27.99
ATOM	573	N	THR	190	41.385	72.251	-9.570	1.00	24.30
ATOM	574	H	THR	190	40.494	72.204	-9.158	1.00	0.00
ATOM	575	CA	THR	190	41.446	72.677	-10.959	1.00	23.16
ATOM	576	CB	THR	190	40.030	73.023	-11.453	1.00	23.46
ATOM	577	OG1	THR	190	39.259	71.861	-11.228	1.00	23.54
ATOM	578	HG1	THR	190	38.355	72.025	-11.500	1.00	0.00
ATOM	579	CG2	THR	190	39.922	73.321	-12.943	1.00	19.04
ATOM	580	C	THR	190	42.363	73.878	-11.143	1.00	25.40
ATOM	581	O	THR	190	43.255	73.913	-11.989	1.00	25.28
ATOM	582	N	MET	191	42.207	74.935	-10.353	1.00	25.85
ATOM	583	H	MET	191	41.531	74.956	-9.640	1.00	0.00
ATOM	584	CA	MET	191	43.092	76.058	-10.563	1.00	26.80
ATOM	585	CB	MET	191	42.618	77.263	-9.731	1.00	31.82
ATOM	586	CG	MET	191	41.203	77.811	-10.021	1.00	30.18
ATOM	587	SD	MET	191	40.720	77.816	-11.767	1.00	42.05
ATOM	588	CE	MET	191	42.005	78.898	-12.322	1.00	40.61
ATOM	589	C	MET	191	44.534	75.727	-10.227	1.00	26.94
ATOM	590	O	MET	191	45.439	76.102	-10.949	1.00	28.00
ATOM	591	N	LEU	192	44.841	75.015	-9.139	1.00	25.81
ATOM	592	H	LEU	192	44.141	74.785	-8.487	1.00	0.00
ATOM	593	CA	LEU	192	46.207	74.599	-8.872	1.00	22.18
ATOM	594	CB	LEU	192	46.226	73.695	-7.637	1.00	19.29
ATOM	595	CG	LEU	192	47.592	73.125	-7.246	1.00	25.33
ATOM	596	CD1	LEU	192	48.470	74.276	-6.797	1.00	25.29
ATOM	597	CD2	LEU	192	47.450	72.049	-6.153	1.00	25.35
ATOM	598	C	LEU	192	46.798	73.872	-10.049	1.00	19.90
ATOM	599	O	LEU	192	47.871	74.187	-10.546	1.00	19.35
ATOM	600	N	LEU	193	46.115	72.857	-10.554	1.00	20.99
ATOM	601	H	LEU	193	45.208	72.654	-10.237	1.00	0.00
ATOM	602	CA	LEU	193	46.743	72.049	-11.571	1.00	21.52
ATOM	603	CB	LEU	193	45.920	70.802	-11.849	1.00	21.31
ATOM	604	CG	LEU	193	46.081	69.749	-10.749	1.00	23.69
ATOM	605	CD1	LEU	193	45.125	68.587	-11.000	1.00	26.09
ATOM	606	CD2	LEU	193	47.509	69.236	-10.751	1.00	24.27
ATOM	607	C	LEU	193	46.921	72.815	-12.844	1.00	25.18
ATOM	608	O	LEU	193	47.962	72.768	-13.484	1.00	25.97
ATOM	609	N	GLN	194	45.909	73.565	-13.262	1.00	27.74
ATOM	610	H	GLN	194	45.038	73.515	-12.809	1.00	0.00
ATOM	611	CA	GLN	194	46.071	74.455	-14.391	1.00	29.82
ATOM	612	CB	GLN	194	44.769	75.244	-14.530	1.00	28.29
ATOM	613	CG	GLN	194	44.400	75.460	-15.983	1.00	33.28
ATOM	614	CD	GLN	194	42.994	75.954	-16.101	1.00	34.79
ATOM	615	OE1	GLN	194	42.085	75.270	-16.546	1.00	33.62
ATOM	616	NE2	GLN	194	42.733	77.202	-15.779	1.00	36.58
ATOM	617	HE21	GLN	194	43.468	77.783	-15.495	1.00	0.00
ATOM	618	HE22	GLN	194	41.799	77.487	-15.861	1.00	0.00
ATOM	619	C	GLN	194	47.281	75.347	-14.146	1.00	31.33
ATOM	620	O	GLN	194	48.177	75.481	-14.964	1.00	31.54
ATOM	621	N	ASN	195	47.356	75.986	-12.990	1.00	33.01
ATOM	622	H	ASN	195	46.613	75.928	-12.354	1.00	0.00
ATOM	623	CA	ASN	195	48.530	76.762	-12.606	1.00	30.77
ATOM	624	CB	ASN	195	48.460	77.239	-11.151	1.00	34.88
ATOM	625	CG	ASN	195	47.691	78.525	-10.957	1.00	38.35
ATOM	626	OD1	ASN	195	47.679	79.452	-11.753	1.00	43.57
ATOM	627	ND2	ASN	195	47.015	78.668	-9.836	1.00	36.28
ATOM	628	HD21	ASN	195	47.044	77.925	-9.206	1.00	0.00
ATOM	629	HD22	ASN	195	46.506	79.497	-9.715	1.00	0.00
ATOM	630	C	ASN	195	49.860	76.066	-12.719	1.00	28.51
ATOM	631	O	ASN	195	50.871	76.696	-12.949	1.00	26.10

ATOM	632	N	LEU	196	49.928	74.758	-12.542	1.00	27.38
ATOM	633	H	LEU	196	49.112	74.264	-12.313	1.00	0.00
ATOM	634	CA	LEU	196	51.193	74.051	-12.683	1.00	25.33
ATOM	635	CB	LEU	196	51.179	72.795	-11.806	1.00	24.19
ATOM	636	CG	LEU	196	51.188	73.150	-10.326	1.00	23.30
ATOM	637	CD1	LEU	196	50.972	71.914	-9.481	1.00	24.60
ATOM	638	CD2	LEU	196	52.519	73.794	-9.985	1.00	31.63
ATOM	639	C	LEU	196	51.433	73.661	-14.123	1.00	26.23
ATOM	640	O	LEU	196	52.442	73.078	-14.503	1.00	24.03
ATOM	641	N	GLY	197	50.478	73.970	-14.993	1.00	27.17
ATOM	642	H	GLY	197	49.631	74.363	-14.695	1.00	0.00
ATOM	643	CA	GLY	197	50.704	73.779	-16.401	1.00	25.75
ATOM	644	C	GLY	197	49.860	72.707	-17.015	1.00	26.04
ATOM	645	O	GLY	197	50.142	72.320	-18.140	1.00	27.75
ATOM	646	N	TYR	198	48.830	72.188	-16.360	1.00	24.74
ATOM	647	H	TYR	198	48.531	72.597	-15.518	1.00	0.00
ATOM	648	CA	TYR	198	48.125	71.016	-16.872	1.00	24.17
ATOM	649	CB	TYR	198	47.870	69.968	-15.744	1.00	24.44
ATOM	650	CG	TYR	198	49.145	69.319	-15.195	1.00	17.56
ATOM	651	CD1	TYR	198	49.919	69.969	-14.251	1.00	17.53
ATOM	652	CE1	TYR	198	51.123	69.433	-13.835	1.00	19.28
ATOM	653	CD2	TYR	198	49.572	68.117	-15.711	1.00	16.54
ATOM	654	CE2	TYR	198	50.771	67.572	-15.298	1.00	17.99
ATOM	655	CZ	TYR	198	51.567	68.265	-14.399	1.00	22.77
ATOM	656	OH	TYR	198	52.806	67.774	-14.022	1.00	26.91
ATOM	657	HH	TYR	198	53.179	68.383	-13.376	1.00	0.00
ATOM	658	C	TYR	198	46.794	71.385	-17.465	1.00	25.30
ATOM	659	O	TYR	198	46.136	72.288	-16.959	1.00	28.39
ATOM	660	N	SER	199	46.353	70.714	-18.533	1.00	27.93
ATOM	661	H	SER	199	46.951	70.163	-19.092	1.00	0.00
ATOM	662	CA	SER	199	44.953	70.775	-18.924	1.00	29.13
ATOM	663	CB	SER	199	44.776	70.400	-20.402	1.00	31.52
ATOM	664	OG	SER	199	45.617	71.216	-21.197	1.00	44.44
ATOM	665	HG	SER	199	45.356	72.131	-21.040	1.00	0.00
ATOM	666	C	SER	199	44.163	69.810	-18.077	1.00	25.88
ATOM	667	O	SER	199	44.489	68.636	-17.967	1.00	28.99
ATOM	668	N	VAL	200	43.095	70.325	-17.471	1.00	22.17
ATOM	669	H	VAL	200	42.823	71.240	-17.708	1.00	0.00
ATOM	670	CA	VAL	200	42.321	69.612	-16.481	1.00	21.46
ATOM	671	CB	VAL	200	42.090	70.526	-15.284	1.00	17.18
ATOM	672	CG1	VAL	200	41.528	69.691	-14.142	1.00	19.27
ATOM	673	CG2	VAL	200	43.399	71.222	-14.885	1.00	17.36
ATOM	674	C	VAL	200	40.978	69.116	-16.979	1.00	25.60
ATOM	675	O	VAL	200	40.073	69.889	-17.248	1.00	26.95
ATOM	676	N	ASP	201	40.787	67.815	-17.115	1.00	25.10
ATOM	677	H	ASP	201	41.548	67.209	-17.020	1.00	0.00
ATOM	678	CA	ASP	201	39.459	67.259	-17.292	1.00	26.46
ATOM	679	CB	ASP	201	39.501	65.852	-17.808	1.00	32.29
ATOM	680	CG	ASP	201	39.387	65.818	-19.271	1.00	40.02
ATOM	681	OD1	ASP	201	38.413	65.246	-19.737	1.00	53.36
ATOM	682	OD2	ASP	201	40.251	66.358	-19.949	1.00	48.96
ATOM	683	C	ASP	201	38.786	67.159	-15.940	1.00	28.68
ATOM	684	O	ASP	201	39.402	66.593	-15.030	1.00	25.09
ATOM	685	N	VAL	202	37.561	67.665	-15.755	1.00	26.15
ATOM	686	H	VAL	202	37.092	68.158	-16.463	1.00	0.00
ATOM	687	CA	VAL	202	36.820	67.390	-14.543	1.00	29.60
ATOM	688	CB	VAL	202	36.274	68.690	-13.955	1.00	29.43
ATOM	689	CG1	VAL	202	35.461	68.387	-12.696	1.00	26.97
ATOM	690	CG2	VAL	202	37.434	69.634	-13.649	1.00	26.15
ATOM	691	C	VAL	202	35.669	66.447	-14.865	1.00	33.37
ATOM	692	O	VAL	202	34.893	66.731	-15.763	1.00	36.29
ATOM	693	N	LYS	203	35.496	65.309	-14.183	1.00	33.12
ATOM	694	H	LYS	203	36.163	65.050	-13.508	1.00	0.00
ATOM	695	CA	LYS	203	34.334	64.448	-14.372	1.00	28.52

ATOM	696	CB	LYS	203	34.749	63.050	-14.826	1.00	28.62
ATOM	697	CG	LYS	203	35.590	62.990	-16.088	1.00	32.11
ATOM	698	CD	LYS	203	34.746	63.437	-17.266	1.00	40.39
ATOM	699	CE	LYS	203	35.531	63.532	-18.574	1.00	50.57
ATOM	700	NZ	LYS	203	34.651	64.012	-19.625	1.00	59.39
ATOM	701	HZ1	LYS	203	34.274	64.946	-19.364	1.00	0.00
ATOM	702	HZ2	LYS	203	33.854	63.352	-19.738	1.00	0.00
ATOM	703	HZ3	LYS	203	35.168	64.088	-20.524	1.00	0.00
ATOM	704	C	LYS	203	33.596	64.313	-13.046	1.00	29.68
ATOM	705	O	LYS	203	34.220	64.117	-12.016	1.00	30.93
ATOM	706	N	LYS	204	32.268	64.402	-12.954	1.00	32.55
ATOM	707	H	LYS	204	31.711	64.391	-13.762	1.00	0.00
ATOM	708	CA	LYS	204	31.610	64.417	-11.655	1.00	34.17
ATOM	709	CB	LYS	204	30.827	65.701	-11.363	1.00	32.07
ATOM	710	CG	LYS	204	31.646	66.950	-11.553	1.00	37.18
ATOM	711	CD	LYS	204	30.858	68.196	-11.188	1.00	44.8
ATOM	712	CE	LYS	204	31.660	69.462	-11.544	1.00	54.50
ATOM	713	NZ	LYS	204	30.997	70.674	-11.086	1.00	60.66
ATOM	714	HZ1	LYS	204	30.884	70.631	-10.052	1.00	0.00
ATOM	715	HZ2	LYS	204	30.058	70.742	-11.528	1.00	0.00
ATOM	716	HZ3	LYS	204	31.568	71.505	-11.339	1.00	0.00
ATOM	717	C	LYS	204	30.603	63.311	-11.602	1.00	32.66
ATOM	718	O	LYS	204	30.073	62.894	-12.625	1.00	33.79
ATOM	719	N	ASN	205	30.378	62.866	-10.365	1.00	31.17
ATOM	720	H	ASN	205	30.983	63.186	-9.659	1.00	0.00
ATOM	721	CA	ASN	205	29.340	61.902	-10.003	1.00	29.81
ATOM	722	CB	ASN	205	27.956	62.531	-10.122	1.00	25.29
ATOM	723	CG	ASN	205	27.915	63.623	-9.103	1.00	26.48
ATOM	724	OD1	ASN	205	28.416	63.536	-7.988	1.00	29.97
ATOM	725	ND2	ASN	205	27.363	64.768	-9.456	1.00	29.11
ATOM	726	HD21	ASN	205	27.014	64.830	-10.369	1.00	0.00
ATOM	727	HD22	ASN	205	27.318	65.493	-8.798	1.00	0.00
ATOM	728	C	ASN	205	29.323	60.626	-10.792	1.00	30.34
ATOM	729	O	ASN	205	28.356	60.317	-11.453	1.00	32.35
ATOM	730	N	LEU	206	30.354	59.799	-10.793	1.00	31.19
ATOM	731	H	LEU	206	31.092	59.947	-10.163	1.00	0.00
ATOM	732	CA	LEU	206	30.352	58.667	-11.698	1.00	28.61
ATOM	733	CB	LEU	206	31.657	58.587	-12.498	1.00	29.20
ATOM	734	CG	LEU	206	32.070	59.852	-13.281	1.00	29.46
ATOM	735	CD1	LEU	206	33.375	59.557	-14.009	1.00	30.38
ATOM	736	CD2	LEU	206	31.010	60.255	-14.297	1.00	33.07
ATOM	737	C	LEU	206	30.196	57.402	-10.933	1.00	30.76
ATOM	738	O	LEU	206	30.211	57.314	-9.715	1.00	35.60
ATOM	739	N	THR	207	30.043	56.331	-11.664	1.00	32.87
ATOM	740	H	THR	207	29.939	56.423	-12.631	1.00	0.00
ATOM	741	CA	THR	207	30.012	55.027	-11.058	1.00	36.34
ATOM	742	CB	THR	207	28.851	54.344	-11.773	1.00	36.91
ATOM	743	OG1	THR	207	27.728	54.701	-10.986	1.00	42.24
ATOM	744	HG1	THR	207	26.926	54.355	-11.394	1.00	0.00
ATOM	745	CG2	THR	207	28.942	52.841	-11.905	1.00	42.72
ATOM	746	C	THR	207	31.381	54.358	-11.219	1.00	36.64
ATOM	747	O	THR	207	32.157	54.742	-12.079	1.00	39.32
ATOM	748	N	ALA	208	31.747	53.344	-10.429	1.00	36.10
ATOM	749	H	ALA	208	31.129	53.028	-9.745	1.00	0.00
ATOM	750	CA	ALA	208	33.047	52.699	-10.537	1.00	34.66
ATOM	751	CB	ALA	208	33.042	51.453	-9.643	1.00	32.92
ATOM	752	C	ALA	208	33.402	52.325	-11.959	1.00	36.07
ATOM	753	O	ALA	208	34.525	52.467	-12.425	1.00	38.58
ATOM	754	N	SER	209	32.419	51.840	-12.707	1.00	38.40
ATOM	755	H	SER	209	31.516	51.718	-12.349	1.00	0.00
ATOM	756	CA	SER	209	32.623	51.470	-14.096	1.00	38.81
ATOM	757	CB	SER	209	31.471	50.593	-14.573	1.00	45.07
ATOM	758	OG	SER	209	30.259	51.040	-13.965	1.00	56.06
ATOM	759	HG	SER	209	29.534	50.500	-14.307	1.00	0.00

ATOM	760	C	SER	209	32.724	52.676	-14.978	1.00	35.05
ATOM	761	O	SER	209	33.571	52.733	-15.857	1.00	36.86
ATOM	762	N	ASP	210	31.877	53.687	-14.779	1.00	33.45
ATOM	763	H	ASP	210	31.138	53.563	-14.150	1.00	0.00
ATOM	764	CA	ASP	210	32.061	54.930	-15.516	1.00	36.67
ATOM	765	CB	ASP	210	31.103	56.049	-15.088	1.00	43.07
ATOM	766	CG	ASP	210	29.602	55.780	-15.228	1.00	51.26
ATOM	767	OD1	ASP	210	29.209	54.945	-16.060	1.00	52.07
ATOM	768	OD2	ASP	210	28.830	56.441	-14.507	1.00	50.26
ATOM	769	C	ASP	210	33.469	55.432	-15.219	1.00	36.66
ATOM	770	O	ASP	210	34.155	55.935	-16.096	1.00	34.14
ATOM	771	N	MET	211	33.944	55.299	-13.965	1.00	36.25
ATOM	772	H	MET	211	33.371	54.919	-13.268	1.00	0.00
ATOM	773	CA	MET	211	35.310	55.693	-13.629	1.00	36.30
ATOM	774	CB	MET	211	35.574	55.528	-12.130	1.00	32.55
ATOM	775	CG	MET	211	34.914	56.611	-11.271	1.00	31.33
ATOM	776	SD	MET	211	35.182	56.360	-9.493	1.00	38.31
ATOM	777	CE	MET	211	34.219	57.715	-8.954	1.00	38.56
ATOM	778	C	MET	211	36.310	54.866	-14.404	1.00	33.55
ATOM	779	O	MET	211	37.247	55.382	-14.999	1.00	35.45
ATOM	780	N	THR	212	36.140	53.551	-14.436	1.00	30.54
ATOM	781	H	THR	212	35.445	53.118	-13.893	1.00	0.00
ATOM	782	CA	THR	212	36.997	52.704	-15.242	1.00	31.66
ATOM	783	CB	THR	212	36.443	51.289	-15.170	1.00	30.49
ATOM	784	OG1	THR	212	36.580	50.901	-13.805	1.00	36.43
ATOM	785	HG1	THR	212	37.491	50.999	-13.515	1.00	0.00
ATOM	786	CG2	THR	212	37.128	50.325	-16.127	1.00	30.70
ATOM	787	C	THR	212	37.122	53.142	-16.681	1.00	30.78
ATOM	788	O	THR	212	38.195	53.275	-17.241	1.00	30.06
ATOM	789	N	THR	213	35.973	53.375	-17.297	1.00	34.48
ATOM	790	H	THR	213	35.126	53.245	-16.813	1.00	0.00
ATOM	791	CA	THR	213	35.869	53.796	-18.681	1.00	33.70
ATOM	792	CB	THR	213	34.354	53.892	-19.044	1.00	38.71
ATOM	793	OG1	THR	213	33.818	52.581	-18.856	1.00	42.49
ATOM	794	HG1	THR	213	34.273	51.966	-19.436	1.00	0.00
ATOM	795	CG2	THR	213	34.086	54.420	-20.467	1.00	40.74
ATOM	796	C	THR	213	36.571	55.122	-18.900	1.00	31.43
ATOM	797	O	THR	213	37.304	55.298	-19.865	1.00	30.44
ATOM	798	N	GLU	214	36.356	56.097	-18.006	1.00	29.82
ATOM	799	H	GLU	214	35.706	55.963	-17.279	1.00	0.00
ATOM	800	CA	GLU	214	37.082	57.351	-18.103	1.00	29.65
ATOM	801	CB	GLU	214	36.673	58.355	-17.025	1.00	33.21
ATOM	802	CG	GLU	214	35.275	58.972	-17.161	1.00	39.44
ATOM	803	CD	GLU	214	34.998	59.508	-18.559	1.00	44.47
ATOM	804	OE1	GLU	214	35.754	60.353	-19.052	1.00	46.83
ATOM	805	OE2	GLU	214	34.015	59.057	-19.154	1.00	48.55
ATOM	806	C	GLU	214	38.561	57.147	-17.960	1.00	26.00
ATOM	807	O	GLU	214	39.348	57.759	-18.665	1.00	23.58
ATOM	808	N	LEU	215	38.976	56.276	-17.045	1.00	26.22
ATOM	809	H	LEU	215	38.327	55.881	-16.422	1.00	0.00
ATOM	810	CA	LEU	215	40.392	55.922	-16.942	1.00	30.25
ATOM	811	CB	LEU	215	40.670	54.929	-15.786	1.00	28.64
ATOM	812	CG	LEU	215	40.608	55.547	-14.386	1.00	31.22
ATOM	813	CD1	LEU	215	40.822	54.470	-13.329	1.00	30.89
ATOM	814	CD2	LEU	215	41.648	56.656	-14.292	1.00	24.41
ATOM	815	C	LEU	215	40.966	55.300	-18.190	1.00	29.50
ATOM	816	O	LEU	215	41.998	55.738	-18.686	1.00	32.89
ATOM	817	N	GLU	216	40.334	54.261	-18.740	1.00	27.46
ATOM	818	H	GLU	216	39.555	53.884	-18.282	1.00	0.00
ATOM	819	CA	GLU	216	40.802	53.695	-19.991	1.00	30.27
ATOM	820	CB	GLU	216	39.922	52.537	-20.463	1.00	38.22
ATOM	821	CG	GLU	216	39.940	51.319	-19.517	1.00	54.67
ATOM	822	CD	GLU	216	39.089	50.173	-20.064	1.00	60.29
ATOM	823	OE1	GLU	216	39.535	49.546	-21.027	1.00	63.24

ATOM	824	OE2	GLU	216	38.003	49.907	-19.525	1.00	60.46
ATOM	825	C	GLU	216	40.823	54.724	-21.094	1.00	29.88
ATOM	826	O	GLU	216	41.722	54.757	-21.926	1.00	27.84
ATOM	827	N	ALA	217	39.836	55.617	-21.144	1.00	27.72
ATOM	828	H	ALA	217	39.086	55.550	-20.516	1.00	0.00
ATOM	829	CA	ALA	217	39.851	56.698	-22.121	1.00	27.12
ATOM	830	CB	ALA	217	38.530	57.477	-22.045	1.00	27.01
ATOM	831	C	ALA	217	41.008	57.620	-21.855	1.00	26.62
ATOM	832	O	ALA	217	41.791	57.934	-22.740	1.00	26.18
ATOM	833	N	PHE	218	41.179	58.083	-20.624	1.00	25.15
ATOM	834	H	PHE	218	40.554	57.809	-19.917	1.00	0.00
ATOM	835	CA	PHE	218	42.258	58.999	-20.319	1.00	23.19
ATOM	836	CB	PHE	218	42.185	59.322	-18.828	1.00	20.84
ATOM	837	CG	PHE	218	43.236	60.340	-18.445	1.00	25.38
ATOM	838	CD1	PHE	218	44.361	59.929	-17.742	1.00	24.12
ATOM	839	CD2	PHE	218	43.036	61.686	-18.721	1.00	23.15
ATOM	840	CE1	PHE	218	45.234	60.889	-17.262	1.00	23.97
ATOM	841	CE2	PHE	218	43.920	62.634	-18.228	1.00	23.08
ATOM	842	CZ	PHE	218	45.005	62.234	-17.484	1.00	21.26
ATOM	843	C	PHE	218	43.603	58.427	-20.701	1.00	25.14
ATOM	844	O	PHE	218	44.495	59.110	-21.209	1.00	29.00
ATOM	845	N	ALA	219	43.772	57.138	-20.456	1.00	23.61
ATOM	846	H	ALA	219	43.083	56.655	-19.953	1.00	0.00
ATOM	847	CA	ALA	219	44.971	56.429	-20.858	1.00	24.15
ATOM	848	CB	ALA	219	44.884	54.979	-20.375	1.00	24.62
ATOM	849	C	ALA	219	45.224	56.436	-22.351	1.00	30.25
ATOM	850	O	ALA	219	46.335	56.291	-22.834	1.00	30.75
ATOM	851	N	HIS	220	44.155	56.608	-23.131	1.00	31.80
ATOM	852	H	HIS	220	43.276	56.759	-22.722	1.00	0.00
ATOM	853	CA	HIS	220	44.260	56.691	-24.578	1.00	32.54
ATOM	854	CB	HIS	220	43.030	56.108	-25.287	1.00	33.65
ATOM	855	CG	HIS	220	43.153	54.627	-25.144	1.00	38.22
ATOM	856	CD2	HIS	220	43.712	53.790	-26.069	1.00	40.87
ATOM	857	ND1	HIS	220	42.884	53.894	-24.069	1.00	2.77
ATOM	858	HD1	HIS	220	42.460	54.202	-23.244	1.00	0.00
ATOM	859	CE1	HIS	220	43.283	52.673	-24.281	1.00	41.06
ATOM	860	NE2	HIS	220	43.788	52.624	-25.483	1.00	39.69
ATOM	861	HE2	HIS	220	44.189	51.815	-25.855	1.00	0.00
ATOM	862	C	HIS	220	44.431	58.066	-25.139	1.00	31.27
ATOM	863	O	HIS	220	44.482	58.222	-26.346	1.00	34.54
ATOM	864	N	ARG	221	44.519	59.129	-24.354	1.00	31.23
ATOM	865	H	ARG	221	44.453	59.018	-23.381	1.00	0.00
ATOM	866	CA	ARG	221	44.684	60.441	-24.935	1.00	25.20
ATOM	867	CB	ARG	221	44.496	61.460	-23.847	1.00	23.87
ATOM	868	CG	ARG	221	43.089	61.433	-23.298	1.00	24.28
ATOM	869	CD	ARG	221	42.164	62.262	-24.150	1.00	24.77
ATOM	870	NE	ARG	221	42.527	63.666	-24.117	1.00	30.34
ATOM	871	HE	ARG	221	43.163	64.003	-24.780	1.00	0.00
ATOM	872	CZ	ARG	221	42.025	64.537	-23.214	1.00	36.39
ATOM	873	NH1	ARG	221	41.323	64.137	-22.120	1.00	37.62
ATOM	874	HH11	ARG	221	41.185	63.163	-21.950	1.00	0.00
ATOM	875	HH12	ARG	221	40.981	64.814	-21.467	1.00	0.00
ATOM	876	NH2	ARG	221	42.162	65.884	-23.412	1.00	36.36
ATOM	877	HH21	ARG	221	42.631	66.223	-24.228	1.00	0.00
ATOM	878	HH22	ARG	221	41.797	66.529	-22.740	1.00	0.00
ATOM	879	C	ARG	221	46.030	60.643	-25.605	1.00	27.94
ATOM	880	O	ARG	221	47.097	60.475	-25.015	1.00	27.32
ATOM	881	N	PRO	222	46.015	61.030	-26.842	1.00	30.14
ATOM	882	CD	PRO	222	44.795	61.277	-27.621	1.00	28.66
ATOM	883	CA	PRO	222	47.204	61.317	-27.635	1.00	26.80
ATOM	884	CB	PRO	222	46.670	61.799	-28.976	1.00	27.03
ATOM	885	CG	PRO	222	45.279	62.298	-28.634	1.00	26.07
ATOM	886	C	PRO	222	48.125	62.326	-26.990	1.00	28.33
ATOM	887	O	PRO	222	49.329	62.305	-27.184	1.00	34.07

ATOM	888	N	GLU	223	47.627	63.254	-26.189	1.00	25.34
ATOM	889	H	GLU	223	46.669	63.259	-26.005	1.00	0.00
ATOM	890	CA	GLU	223	48.500	64.265	-25.620	1.00	28.40
ATOM	891	CB	GLU	223	47.671	65.306	-24.887	1.00	27.51
ATOM	892	CG	GLU	223	46.658	66.030	-25.769	1.00	32.04
ATOM	893	CD	GLU	223	45.293	65.381	-25.726	1.00	34.72
ATOM	894	OE1	GLU	223	44.328	66.114	-25.534	1.00	35.25
ATOM	895	OE2	GLU	223	45.177	64.168	-25.880	1.00	38.35
ATOM	896	C	GLU	223	49.569	63.758	-24.663	1.00	28.17
ATOM	897	O	GLU	223	50.606	64.371	-24.461	1.00	28.18
ATOM	898	N	HIS	224	49.343	62.599	-24.034	1.00	26.29
ATOM	899	H	HIS	224	48.522	62.108	-24.230	1.00	0.00
ATOM	900	CA	HIS	224	50.346	62.037	-23.139	1.00	25.11
ATOM	901	CB	HIS	224	49.960	60.670	-22.601	1.00	21.67
ATOM	902	CG	HIS	224	48.774	60.779	-21.676	1.00	28.93
ATOM	903	CD2	HIS	224	47.721	59.901	-21.673	1.00	29.23
ATOM	904	ND1	HIS	224	48.546	61.704	-20.722	1.00	26.59
ATOM	905	HD1	HIS	224	49.236	62.337	-20.408	1.00	0.00
ATOM	906	CE1	HIS	224	47.382	61.423	-20.177	1.00	31.44
ATOM	907	NE2	HIS	224	46.889	60.352	-20.773	1.00	33.43
ATOM	908	HE2	HIS	224	46.004	59.939	-20.625	1.00	0.00
ATOM	909	C	HIS	224	51.646	61.845	-23.859	1.00	26.89
ATOM	910	O	HIS	224	52.700	62.029	-23.281	1.00	30.62
ATOM	911	N	LYS	225	51.608	61.474	-25.138	1.00	30.81
ATOM	912	H	LYS	225	50.750	61.290	-25.584	1.00	0.00
ATOM	913	CA	LYS	225	52.826	61.359	-25.937	1.00	32.77
ATOM	914	CB	LYS	225	52.503	60.985	-27.373	1.00	39.91
ATOM	915	CG	LYS	225	52.645	59.492	-27.564	1.00	55.31
ATOM	916	CD	LYS	225	52.548	59.057	-29.024	1.00	67.66
ATOM	917	CE	LYS	225	52.571	57.524	-29.181	1.00	75.00
ATOM	918	NZ	LYS	225	51.337	56.917	-28.699	1.00	78.51
ATOM	919	HZ1	LYS	225	50.529	57.292	-29.236	1.00	0.00
ATOM	920	HZ2	LYS	225	51.211	57.140	-27.691	1.00	0.00
ATOM	921	HZ3	LYS	225	51.387	55.887	-28.827	1.00	0.00
ATOM	922	C	LYS	225	53.638	62.627	-25.985	1.00	30.17
ATOM	923	O	LYS	225	54.854	62.599	-26.051	1.00	32.06
ATOM	924	N	THR	226	53.015	63.792	-25.975	1.00	29.27
ATOM	925	H	THR	226	52.045	63.869	-26.061	1.00	0.00
ATOM	926	CA	THR	226	53.803	64.992	-25.854	1.00	29.35
ATOM	927	CB	THR	226	53.293	66.018	-26.896	1.00	28.73
ATOM	928	OG1	THR	226	51.944	65.709	-27.203	1.00	27.05
ATOM	929	HG1	THR	226	51.452	66.009	-26.422	1.00	0.00
ATOM	930	CG2	THR	226	54.127	65.983	-28.180	1.00	31.09
ATOM	931	C	THR	226	53.770	65.546	-24.441	1.00	30.98
ATOM	932	O	THR	226	53.809	66.756	-24.226	1.00	34.36
ATOM	933	N	SER	227	53.685	64.702	-23.408	1.00	27.84
ATOM	934	H	SER	227	53.657	63.727	-23.528	1.00	0.00
ATOM	935	CA	SER	227	53.733	65.196	-22.055	1.00	25.31
ATOM	936	CB	SER	227	52.412	64.917	-21.322	1.00	23.69
ATOM	937	OG	SER	227	52.319	65.533	-20.021	1.00	29.36
ATOM	938	HG	SER	227	51.584	65.178	-19.486	1.00	0.00
ATOM	939	C	SER	227	54.872	64.535	-21.301	1.00	27.92
ATOM	940	O	SER	227	55.409	63.498	-21.661	1.00	22.67
ATOM	941	N	ASP	228	55.246	65.201	-20.199	1.00	28.65
ATOM	942	H	ASP	228	54.753	66.020	-19.977	1.00	0.00
ATOM	943	CA	ASP	228	56.270	64.715	-19.270	1.00	28.62
ATOM	944	CB	ASP	228	57.305	65.848	-18.973	1.00	21.37
ATOM	945	CG	ASP	228	56.663	67.095	-18.438	1.00	23.40
ATOM	946	OD1	ASP	228	57.311	68.115	-18.499	1.00	25.53
ATOM	947	OD2	ASP	228	55.524	67.071	-17.976	1.00	24.44
ATOM	948	C	ASP	228	55.732	64.156	-17.923	1.00	29.79
ATOM	949	O	ASP	228	56.509	63.644	-17.121	1.00	33.42
ATOM	950	N	SER	229	54.425	64.213	-17.599	1.00	30.06
ATOM	951	H	SER	229	53.756	64.595	-18.213	1.00	0.00

ATOM	952	CA	SER	229	53.905	63.708	-16.336	1.00	24.85
ATOM	953	CB	SER	229	54.314	64.599	-15.182	1.00	21.77
ATOM	954	OG	SER	229	54.171	65.969	-15.547	1.00	21.06
ATOM	955	HG	SER	229	54.272	66.564	-14.792	1.00	0.00
ATOM	956	C	SER	229	52.413	63.747	-16.437	1.00	23.31
ATOM	957	O	SER	229	51.900	64.273	-17.423	1.00	23.18
ATOM	958	N	THR	230	51.720	63.201	-15.435	1.00	24.93
ATOM	959	H	THR	230	52.164	62.618	-14.780	1.00	0.00
ATOM	960	CA	THR	230	50.303	63.473	-15.239	1.00	22.17
ATOM	961	CB	THR	230	49.501	62.410	-16.052	1.00	18.90
ATOM	962	OG1	THR	230	48.158	62.903	-16.198	1.00	23.08
ATOM	963	HG1	THR	230	48.158	63.784	-16.611	1.00	0.00
ATOM	964	CG2	THR	230	49.485	61.030	-15.391	1.00	17.19
ATOM	965	C	THR	230	49.933	63.471	-13.739	1.00	22.19
ATOM	966	O	THR	230	50.683	63.015	-12.887	1.00	19.95
ATOM	967	N	PHE	231	48.751	63.999	-13.412	1.00	23.01
ATOM	968	H	PHE	231	48.196	64.345	-14.142	1.00	0.00
ATOM	969	CA	PHE	231	48.168	64.022	-12.081	1.00	22.98
ATOM	970	CB	PHE	231	47.955	65.441	-11.549	1.00	22.01
ATOM	971	CG	PHE	231	49.190	65.978	-10.873	1.00	23.66
ATOM	972	CD1	PHE	231	49.220	66.071	-9.486	1.00	22.17
ATOM	973	CD2	PHE	231	50.273	66.392	-11.635	1.00	21.19
ATOM	974	CE1	PHE	231	50.361	66.561	-8.861	1.00	23.83
ATOM	975	CE2	PHE	231	51.391	66.900	-11.010	1.00	18.70
ATOM	976	CZ	PHE	231	51.442	66.965	-9.620	1.00	22.93
ATOM	977	C	PHE	231	46.792	63.409	-12.160	1.00	21.75
ATOM	978	O	PHE	231	46.067	63.809	-13.062	1.00	21.91
ATOM	979	N	LEU	232	46.343	62.479	-11.312	1.00	20.85
ATOM	980	H	LEU	232	46.949	62.069	-10.654	1.00	0.00
ATOM	981	CA	LEU	232	44.915	62.139	-11.293	1.00	19.87
ATOM	982	CB	LEU	232	44.627	60.672	-11.588	1.00	23.90
ATOM	983	CG	LEU	232	45.050	60.289	-12.995	1.00	30.22
ATOM	984	CD1	LEU	232	46.486	59.760	-12.956	1.00	32.80
ATOM	985	CD2	LEU	232	44.089	59.240	-13.555	1.00	32.58
ATOM	986	C	LEU	232	44.338	62.387	-9.941	1.00	18.92
ATOM	987	O	LEU	232	44.980	62.002	-8.979	1.00	22.64
ATOM	988	N	VAL	233	43.174	62.998	-9.754	1.00	20.69
ATOM	989	H	VAL	233	42.629	63.238	-10.535	1.00	0.00
ATOM	990	CA	VAL	233	42.664	63.290	-8.423	1.00	22.20
ATOM	991	CB	VAL	233	42.519	64.812	-8.180	1.00	21.39
ATOM	992	CG1	VAL	233	42.185	65.090	-6.706	1.00	20.83
ATOM	993	CG2	VAL	233	43.826	65.525	-8.539	1.00	27.21
ATOM	994	C	VAL	233	41.291	62.645	-8.264	1.00	27.10
ATOM	995	O	VAL	233	40.429	62.803	-9.122	1.00	24.87
ATOM	996	N	PHE	234	41.049	61.906	-7.176	1.00	24.72
ATOM	997	H	PHE	234	41.749	61.801	-6.495	1.00	0.00
ATOM	998	CA	PHE	234	39.764	61.286	-6.938	1.00	23.25
ATOM	999	CB	PHE	234	39.870	59.773	-6.767	1.00	20.01
ATOM	1000	CG	PHE	234	40.400	59.110	-8.005	1.00	21.08
ATOM	1001	CD1	PHE	234	39.525	58.555	-8.904	1.00	26.42
ATOM	1002	CD2	PHE	234	41.768	59.045	-8.222	1.00	25.79
ATOM	1003	CE1	PHE	234	40.019	57.951	-10.046	1.00	29.30
ATOM	1004	CE2	PHE	234	42.262	58.445	-9.353	1.00	23.33
ATOM	1005	CZ	PHE	234	41.379	57.910	-10.266	1.00	31.52
ATOM	1006	C	PHE	234	39.259	61.858	-5.650	1.00	25.38
ATOM	1007	O	PHE	234	39.990	61.926	-4.664	1.00	27.17
ATOM	1008	N	MET	235	38.006	62.298	-5.583	1.00	26.22
ATOM	1009	H	MET	235	37.441	62.301	-6.384	1.00	0.00
ATOM	1010	CA	MET	235	37.451	62.780	-4.326	1.00	25.64
ATOM	1011	CB	MET	235	37.276	64.294	-4.345	1.00	24.45
ATOM	1012	CG	MET	235	38.619	64.946	-4.681	1.00	30.66
ATOM	1013	SD	MET	235	38.601	66.742	-4.848	1.00	37.65
ATOM	1014	CE	MET	235	38.003	66.982	-6.481	1.00	33.32
ATOM	1015	C	MET	235	36.120	62.112	-4.236	1.00	29.15

ATOM	1016	O	MET	235	35.339	62.186	-5.175	1.00	29.75
ATOM	1017	N	SER	236	35.808	61.432	-3.138	1.00	31.99
ATOM	1018	H	SER	236	36.441	61.364	-2.382	1.00	0.00
ATOM	1019	CA	SER	236	34.531	60.769	-2.995	1.00	32.91
ATOM	1020	CB	SER	236	34.412	59.596	-3.971	1.00	31.29
ATOM	1021	OG	SER	236	33.125	58.996	-3.885	1.00	32.86
ATOM	1022	HG	SER	236	32.463	59.641	-4.143	1.00	0.00
ATOM	1023	C	SER	236	34.462	60.246	-1.573	1.00	32.69
ATOM	1024	O	SER	236	35.389	60.340	-0.778	1.00	33.35
ATOM	1025	N	HIS	237	33.329	59.661	-1.203	1.00	33.10
ATOM	1026	H	HIS	237	32.551	59.730	-1.783	1.00	0.00
ATOM	1027	CA	HIS	237	33.332	58.809	-0.016	1.00	34.12
ATOM	1028	CB	HIS	237	31.882	58.331	0.377	1.00	37.00
ATOM	1029	CG	HIS	237	31.079	59.375	1.141	1.00	42.87
ATOM	1030	CD2	HIS	237	29.798	59.740	0.816	1.00	40.88
ATOM	1031	ND1	HIS	237	31.457	60.128	2.188	1.00	41.19
ATOM	1032	HD1	HIS	237	32.325	60.120	2.661	1.00	0.00
ATOM	1033	CE1	HIS	237	30.460	60.934	2.446	1.00	43.14
ATOM	1034	NE2	HIS	237	29.466	60.721	1.609	1.00	42.94
ATOM	1035	HE2	HIS	237	28.639	61.252	1.540	1.00	0.00
ATOM	1036	C	HIS	237	34.194	57.577	-0.321	1.00	33.55
ATOM	1037	O	HIS	237	34.520	57.234	-1.462	1.00	32.97
ATOM	1038	N	GLY	238	34.606	56.852	0.702	1.00	32.27
ATOM	1039	H	GLY	238	34.429	57.073	1.646	1.00	0.00
ATOM	1040	CA	GLY	238	35.369	55.668	0.428	1.00	31.94
ATOM	1041	C	GLY	238	35.217	54.774	1.609	1.00	31.47
ATOM	1042	O	GLY	238	34.874	55.189	2.707	1.00	29.62
ATOM	1043	N	ILE	239	35.475	53.512	1.370	1.00	30.61
ATOM	1044	H	ILE	239	35.767	53.236	0.474	1.00	0.00
ATOM	1045	CA	ILE	239	35.461	52.548	2.439	1.00	36.45
ATOM	1046	CB	ILE	239	34.416	51.450	2.210	1.00	38.77
ATOM	1047	CG2	ILE	239	33.067	52.124	2.180	1.00	42.42
ATOM	1048	CG1	ILE	239	34.645	50.683	0.928	1.00	42.77
ATOM	1049	CD1	ILE	239	33.745	49.470	0.810	1.00	45.44
ATOM	1050	C	ILE	239	36.822	51.930	2.435	1.00	37.10
ATOM	1051	O	ILE	239	37.640	52.175	1.572	1.00	37.25
ATOM	1052	N	ARG	240	37.118	51.076	3.398	1.00	39.29
ATOM	1053	H	ARG	240	36.434	50.847	4.063	1.00	0.00
ATOM	1054	CA	ARG	240	38.428	50.462	3.465	1.00	42.79
ATOM	1055	CB	ARG	240	38.400	49.475	4.647	1.00	45.84
ATOM	1056	CG	ARG	240	39.680	48.660	4.892	1.00	52.68
ATOM	1057	CD	ARG	240	40.939	49.489	5.139	1.00	57.36
ATOM	1058	NE	ARG	240	42.114	48.829	4.594	1.00	60.04
ATOM	1059	HE	ARG	240	42.319	48.953	3.645	1.00	0.00
ATOM	1060	CZ	ARG	240	42.922	48.052	5.327	1.00	66.92
ATOM	1061	NH1	ARG	240	44.059	47.576	4.740	1.00	71.12
ATOM	1062	HH11	ARG	240	44.259	47.811	3.789	1.00	0.00
ATOM	1063	HH12	ARG	240	44.688	46.986	5.247	1.00	0.00
ATOM	1064	NH2	ARG	240	42.657	47.711	6.622	1.00	65.55
ATOM	1065	HH21	ARG	240	41.828	48.040	7.073	1.00	0.00
ATOM	1066	HH22	ARG	240	43.298	47.122	7.115	1.00	0.00
ATOM	1067	C	ARG	240	38.863	49.791	2.164	1.00	41.91
ATOM	1068	O	ARG	240	40.040	49.875	1.864	1.00	39.72
ATOM	1069	N	GLU	241	37.969	49.138	1.389	1.00	46.63
ATOM	1070	H	GLU	241	37.022	49.233	1.606	1.00	0.00
ATOM	1071	CA	GLU	241	38.318	48.416	0.151	1.00	49.66
ATOM	1072	CB	GLU	241	37.185	47.460	-0.280	1.00	58.65
ATOM	1073	CG	GLU	241	37.559	46.447	-1.379	1.00	76.02
ATOM	1074	CD	GLU	241	36.387	45.686	-2.058	1.00	84.57
ATOM	1075	OE1	GLU	241	35.539	46.310	-2.712	1.00	86.53
ATOM	1076	OE2	GLU	241	36.350	44.449	-1.970	1.00	90.34
ATOM	1077	C	GLU	241	38.559	49.403	-1.009	1.00	45.34
ATOM	1078	O	GLU	241	39.236	49.102	-1.985	1.00	45.76
ATOM	1079	N	GLY	242	38.015	50.628	-0.966	1.00	40.75

ATOM	1080	H	GLY	242	37.428	50.949	-0.241	1.00	0.00
ATOM	1081	CA	GLY	242	38.362	51.556	-2.014	1.00	35.23
ATOM	1082	C	GLY	242	37.375	52.679	-2.047	1.00	33.55
ATOM	1083	O	GLY	242	36.694	52.955	-1.071	1.00	32.49
ATOM	1084	N	ILE	243	37.290	53.311	-3.213	1.00	31.51
ATOM	1085	H	ILE	243	37.707	52.888	-3.992	1.00	0.00
ATOM	1086	CA	ILE	243	36.590	54.576	-3.407	1.00	30.20
ATOM	1087	CB	ILE	243	37.364	55.376	-4.511	1.00	31.68
ATOM	1088	CG2	ILE	243	36.739	56.740	-4.856	1.00	28.31
ATOM	1089	CG1	ILE	243	38.749	55.674	-3.963	1.00	31.33
ATOM	1090	CD1	ILE	243	39.643	56.077	-5.135	1.00	35.46
ATOM	1091	C	ILE	243	35.148	54.304	-3.806	1.00	30.26
ATOM	1092	O	ILE	243	34.920	53.418	-4.618	1.00	30.91
ATOM	1093	N	CYS	244	34.151	55.017	-3.276	1.00	29.95
ATOM	1094	H	CYS	244	34.337	55.767	-2.666	1.00	0.00
ATOM	1095	CA	CYS	244	32.774	54.760	-3.652	1.00	31.93
ATOM	1096	CB	CYS	244	31.855	55.223	-2.553	1.00	29.44
ATOM	1097	SG	CYS	244	32.093	54.318	-1.030	1.00	36.45
ATOM	1098	C	CYS	244	32.291	55.415	-4.945	1.00	35.60
ATOM	1099	O	CYS	244	32.427	56.619	-5.169	1.00	34.97
ATOM	1100	N	GLY	245	31.695	54.653	-5.863	1.00	34.56
ATOM	1101	H	GLY	245	31.752	53.680	-5.763	1.00	0.00
ATOM	1102	CA	GLY	245	30.973	55.279	-6.962	1.00	37.28
ATOM	1103	C	GLY	245	29.574	55.745	-6.552	1.00	42.13
ATOM	1104	O	GLY	245	29.085	55.433	-5.470	1.00	41.53
ATOM	1105	N	LYS	246	28.868	56.501	-7.415	1.00	44.81
ATOM	1106	H	LYS	246	29.231	56.669	-8.312	1.00	0.00
ATOM	1107	CA	LYS	246	27.604	57.140	-7.033	1.00	47.47
ATOM	1108	CB	LYS	246	27.040	57.989	-8.186	1.00	46.88
ATOM	1109	CG	LYS	246	26.636	57.098	-9.348	1.00	51.88
ATOM	1110	CD	LYS	246	25.882	57.806	-10.459	1.00	62.88
ATOM	1111	CE	LYS	246	24.560	58.422	-10.000	1.00	69.93
ATOM	1112	NZ	LYS	246	24.007	59.246	-11.063	1.00	76.93
ATOM	1113	HZ1	LYS	246	23.833	58.663	-11.905	1.00	0.00
ATOM	1114	HZ2	LYS	246	24.678	60.006	-11.295	1.00	0.00
ATOM	1115	HZ3	LYS	246	23.112	59.670	-10.742	1.00	0.00
ATOM	1116	C	LYS	246	26.477	56.209	-6.574	1.00	48.40
ATOM	1117	O	LYS	246	25.597	56.538	-5.778	1.00	42.25
ATOM	1118	N	LYS	247	26.479	54.982	-7.079	1.00	45.29
ATOM	1119	H	LYS	247	27.176	54.727	-7.713	1.00	0.00
ATOM	1120	CA	LYS	247	25.465	54.045	-6.685	1.00	49.00
ATOM	1121	CB	LYS	247	25.209	53.130	-7.875	1.00	54.11
ATOM	1122	CG	LYS	247	24.508	53.886	-9.004	1.00	62.74
ATOM	1123	CD	LYS	247	24.243	53.001	-10.220	1.00	72.81
ATOM	1124	CE	LYS	247	23.531	53.721	-11.379	1.00	81.38
ATOM	1125	NZ	LYS	247	23.373	52.835	-12.526	1.00	86.55
ATOM	1126	HZ1	LYS	247	22.808	52.005	-12.261	1.00	0.00
ATOM	1127	HZ2	LYS	247	24.310	52.525	-12.854	1.00	0.00
ATOM	1128	HZ3	LYS	247	22.899	53.347	-13.297	1.00	0.00
ATOM	1129	C	LYS	247	25.856	53.257	-5.450	1.00	49.50
ATOM	1130	O	LYS	247	25.319	52.203	-5.182	1.00	51.73
ATOM	1131	N	HIS	248	26.793	53.661	-4.603	1.00	50.46
ATOM	1132	H	HIS	248	27.235	54.526	-4.728	1.00	0.00
ATOM	1133	CA	HIS	248	27.155	52.799	-3.498	1.00	45.73
ATOM	1134	CB	HIS	248	28.438	53.305	-2.813	1.00	40.60
ATOM	1135	CG	HIS	248	28.924	52.330	-1.737	1.00	36.78
ATOM	1136	CD2	HIS	248	29.411	51.071	-1.973	1.00	33.70
ATOM	1137	ND1	HIS	248	28.983	52.505	-0.416	1.00	38.30
ATOM	1138	HD1	HIS	248	28.728	53.315	0.070	1.00	0.00
ATOM	1139	CE1	HIS	248	29.467	51.412	0.129	1.00	34.58
ATOM	1140	NE2	HIS	248	29.720	50.547	-0.817	1.00	33.39
ATOM	1141	HE2	HIS	248	30.051	49.640	-0.658	1.00	0.00
ATOM	1142	C	HIS	248	26.055	52.703	-2.473	1.00	48.32
ATOM	1143	O	HIS	248	25.591	53.685	-1.918	1.00	44.66

ATOM	1144	N	SER	249	25.626	51.478	-2.198	1.00	53.23
ATOM	1145	H	SER	249	25.852	50.711	-2.770	1.00	0.00
ATOM	1146	CA	SER	249	24.798	51.233	-1.040	1.00	57.14
ATOM	1147	CB	SER	249	23.445	50.596	-1.432	1.00	56.80
ATOM	1148	OG	SER	249	23.488	49.267	-1.938	1.00	58.69
ATOM	1149	HG	SER	249	23.996	49.345	-2.757	1.00	0.00
ATOM	1150	C	SER	249	25.626	50.270	-0.262	1.00	59.00
ATOM	1151	O	SER	249	26.610	49.741	-0.760	1.00	55.94
ATOM	1152	N	GLU	250	25.285	50.003	0.982	1.00	68.05
ATOM	1153	H	GLU	250	24.519	50.460	1.391	1.00	0.00
ATOM	1154	CA	GLU	250	25.982	48.958	1.710	1.00	77.66
ATOM	1155	CB	GLU	250	25.518	48.929	3.169	1.00	85.81
ATOM	1156	CG	GLU	250	25.746	50.253	3.922	1.00	96.97
ATOM	1157	CD	GLU	250	25.505	50.056	5.411	1.00	103.17
ATOM	1158	OE1	GLU	250	25.196	51.045	6.085	1.00	108.23
ATOM	1159	OE2	GLU	250	25.633	48.922	5.895	1.00	105.30
ATOM	1160	C	GLU	250	25.778	47.573	1.115	1.00	77.89
ATOM	1161	O	GLU	250	26.649	46.720	1.119	1.00	78.08
ATOM	1162	N	GLN	251	24.574	47.369	0.595	1.00	77.62
ATOM	1163	H	GLN	251	23.971	48.135	0.546	1.00	0.00
ATOM	1164	CA	GLN	251	24.155	46.078	0.085	1.00	77.63
ATOM	1165	CB	GLN	251	22.616	45.902	0.224	1.00	86.21
ATOM	1166	CG	GLN	251	21.677	47.096	0.015	1.00	97.44
ATOM	1167	CD	GLN	251	21.754	48.076	1.182	1.00	106.14
ATOM	1168	OE1	GLN	251	22.556	49.005	1.219	1.00	112.85
ATOM	1169	NE2	GLN	251	20.940	47.965	2.214	1.00	108.86
ATOM	1170	HE21	GLN	251	20.288	47.236	2.234	1.00	0.00
ATOM	1171	HE22	GLN	251	21.031	48.635	2.926	1.00	0.00
ATOM	1172	C	GLN	251	24.544	45.830	-1.356	1.00	74.59
ATOM	1173	O	GLN	251	24.771	44.704	-1.778	1.00	73.25
ATOM	1174	N	VAL	252	24.636	46.863	-2.185	1.00	70.06
ATOM	1175	H	VAL	252	24.241	47.718	-1.911	1.00	0.00
ATOM	1176	CA	VAL	252	25.375	46.711	-3.425	1.00	66.24
ATOM	1177	CB	VAL	252	24.482	46.902	-4.657	1.00	68.01
ATOM	1178	CG1	VAL	252	25.271	47.177	-5.941	1.00	67.58
ATOM	1179	CG2	VAL	252	23.711	45.600	-4.832	1.00	71.77
ATOM	1180	C	VAL	252	26.466	47.745	-3.424	1.00	60.42
ATOM	1181	O	VAL	252	26.282	48.961	-3.409	1.00	57.54
ATOM	1182	N	PRO	253	27.648	47.275	-3.427	1.00	57.04
ATOM	1183	CD	PRO	253	28.022	45.875	-3.278	1.00	57.51
ATOM	1184	CA	PRO	253	28.812	48.113	-3.455	1.00	53.11
ATOM	1185	CB	PRO	253	29.905	47.251	-2.798	1.00	57.01
ATOM	1186	CG	PRO	253	29.165	46.035	-2.272	1.00	57.83
ATOM	1187	C	PRO	253	29.113	48.551	-4.866	1.00	47.52
ATOM	1188	O	PRO	253	28.988	47.837	-5.853	1.00	45.85
ATOM	1189	N	ASP	254	29.533	49.808	-4.931	1.00	42.76
ATOM	1190	H	ASP	254	29.509	50.376	-4.143	1.00	0.00
ATOM	1191	CA	ASP	254	30.038	50.374	-6.156	1.00	38.48
ATOM	1192	CB	ASP	254	29.051	51.461	-6.580	1.00	36.32
ATOM	1193	CG	ASP	254	29.341	51.949	-7.979	1.00	36.27
ATOM	1194	OD1	ASP	254	28.990	53.090	-8.264	1.00	39.87
ATOM	1195	OD2	ASP	254	29.903	51.204	-8.786	1.00	36.65
ATOM	1196	C	ASP	254	31.400	50.909	-5.739	1.00	35.50
ATOM	1197	O	ASP	254	31.506	52.050	-5.321	1.00	34.98
ATOM	1198	N	ILE	255	32.448	50.092	-5.837	1.00	33.54
ATOM	1199	H	ILE	255	32.350	49.250	-6.329	1.00	0.00
ATOM	1200	CA	ILE	255	33.761	50.400	-5.307	1.00	35.65
ATOM	1201	CB	ILE	255	34.181	49.317	-4.295	1.00	39.66
ATOM	1202	CG2	ILE	255	35.615	49.605	-3.797	1.00	40.81
ATOM	1203	CG1	ILE	255	33.157	49.254	-3.144	1.00	39.28
ATOM	1204	CD1	ILE	255	32.955	50.590	-2.435	1.00	40.52
ATOM	1205	C	ILE	255	34.790	50.453	-6.428	1.00	39.99
ATOM	1206	O	ILE	255	34.826	49.556	-7.258	1.00	40.26
ATOM	1207	N	LEU	256	35.642	51.480	-6.503	1.00	39.89

ATOM	1208	H	LEU	256	35.471	52.284	-5.964	1.00	0.00
ATOM	1209	CA	LEU	256	36.831	51.410	-7.340	1.00	39.66
ATOM	1210	CB	LEU	256	37.066	52.755	-8.074	1.00	38.42
ATOM	1211	CG	LEU	256	38.298	52.842	-8.988	1.00	37.25
ATOM	1212	CD1	LEU	256	38.214	51.825	-10.115	1.00	36.68
ATOM	1213	CD2	LEU	256	38.377	54.245	-9.571	1.00	39.39
ATOM	1214	C	LEU	256	38.022	51.095	-6.407	1.00	38.52
ATOM	1215	O	LEU	256	38.368	51.793	-5.455	1.00	40.24
ATOM	1216	N	GLN	257	38.658	49.977	-6.715	1.00	39.82
ATOM	1217	H	GLN	257	38.308	49.468	-7.488	1.00	0.00
ATOM	1218	CA	GLN	257	39.795	49.436	-5.992	1.00	42.81
ATOM	1219	CB	GLN	257	40.050	48.020	-6.455	1.00	49.86
ATOM	1220	CG	GLN	257	40.720	47.077	-5.487	1.00	62.03
ATOM	1221	CD	GLN	257	39.707	46.054	-5.046	1.00	66.77
ATOM	1222	OE1	GLN	257	38.568	46.361	-4.726	1.00	70.03
ATOM	1223	NE2	GLN	257	40.013	44.767	-5.063	1.00	67.84
ATOM	1224	HE21	GLN	257	40.897	44.483	-5.369	1.00	0.00
ATOM	1225	HE22	GLN	257	39.295	44.174	-4.752	1.00	0.00
ATOM	1226	C	GLN	257	40.991	50.253	-6.300	1.00	43.83
ATOM	1227	O	GLN	257	41.296	50.526	-7.457	1.00	44.09
ATOM	1228	N	LEU	258	41.747	50.678	-5.315	1.00	45.79
ATOM	1229	H	LEU	258	41.461	50.433	-4.414	1.00	0.00
ATOM	1230	CA	LEU	258	42.951	51.468	-5.556	1.00	48.19
ATOM	1231	CB	LEU	258	43.638	51.714	-4.187	1.00	62.23
ATOM	1232	CG	LEU	258	45.178	51.726	-4.015	1.00	71.72
ATOM	1233	CD1	LEU	258	45.742	53.135	-3.795	1.00	65.86
ATOM	1234	CD2	LEU	258	45.495	50.830	-2.809	1.00	80.83
ATOM	1235	C	LEU	258	43.958	50.864	-6.564	1.00	46.26
ATOM	1236	O	LEU	258	44.583	51.564	-7.368	1.00	43.62
ATOM	1237	N	ASN	259	44.214	49.561	-6.654	1.00	41.70
ATOM	1238	H	ASN	259	43.687	48.856	-6.205	1.00	0.00
ATOM	1239	CA	ASN	259	45.197	49.203	-7.648	1.00	41.88
ATOM	1240	CB	ASN	259	46.029	48.071	-7.151	1.00	46.19
ATOM	1241	CG	ASN	259	45.376	46.750	-7.280	1.00	49.87
ATOM	1242	OD1	ASN	259	44.187	46.674	-7.008	1.00	56.41
ATOM	1243	ND2	ASN	259	46.115	45.710	-7.644	1.00	50.33
ATOM	1244	HD21	ASN	259	47.075	45.857	-7.810	1.00	0.00
ATOM	1245	HD22	ASN	259	45.682	44.830	-7.714	1.00	0.00
ATOM	1246	C	ASN	259	44.636	48.900	-9.007	1.00	38.03
ATOM	1247	O	ASN	259	45.417	48.585	-9.896	1.00	35.47
ATOM	1248	N	ALA	260	43.309	48.952	-9.180	1.00	33.64
ATOM	1249	H	ALA	260	42.708	49.000	-8.409	1.00	0.00
ATOM	1250	CA	ALA	260	42.732	48.991	-10.512	1.00	29.46
ATOM	1251	CB	ALA	260	41.224	49.011	-10.356	1.00	25.72
ATOM	1252	C	ALA	260	43.243	50.221	-11.230	1.00	28.23
ATOM	1253	O	ALA	260	43.637	50.176	-12.385	1.00	31.28
ATOM	1254	N	ILE	261	43.255	51.359	-10.532	1.00	28.30
ATOM	1255	H	ILE	261	42.856	51.344	-9.640	1.00	0.00
ATOM	1256	CA	ILE	261	43.812	52.619	-11.027	1.00	25.68
ATOM	1257	CB	ILE	261	43.758	53.698	-9.884	1.00	27.06
ATOM	1258	CG2	ILE	261	44.364	55.014	-10.371	1.00	22.81
ATOM	1259	CG1	ILE	261	42.300	53.941	-9.444	1.00	23.10
ATOM	1260	CD1	ILE	261	42.175	54.847	-8.215	1.00	15.19
ATOM	1261	C	ILE	261	45.246	52.443	-11.516	1.00	27.03
ATOM	1262	O	ILE	261	45.594	52.815	-12.626	1.00	30.14
ATOM	1263	N	PHE	262	46.130	51.861	-10.699	1.00	25.11
ATOM	1264	H	PHE	262	45.832	51.647	-9.791	1.00	0.00
ATOM	1265	CA	PHE	262	47.511	51.582	-11.075	1.00	23.29
ATOM	1266	CB	PHE	262	48.275	50.853	-9.941	1.00	23.94
ATOM	1267	CG	PHE	262	48.795	51.855	-8.914	1.00	22.84
ATOM	1268	CD1	PHE	262	47.919	52.571	-8.110	1.00	26.50
ATOM	1269	CD2	PHE	262	50.147	52.112	-8.831	1.00	22.06
ATOM	1270	CE1	PHE	262	48.402	53.570	-7.279	1.00	29.99
ATOM	1271	CE2	PHE	262	50.619	53.093	-7.974	1.00	24.85

ATOM	1272	CZ	PHE	262	49.756	53.842	-7.209	1.00	20.46
ATOM	1273	C	PHE	262	47.573	50.725	-12.288	1.00	27.29
ATOM	1274	O	PHE	262	48.285	50.994	-13.247	1.00	29.20
ATOM	1275	N	ASN	263	46.796	49.640	-12.270	1.00	29.26
ATOM	1276	H	ASN	263	46.219	49.470	-11.496	1.00	0.00
ATOM	1277	CA	ASN	263	46.827	48.683	-13.372	1.00	32.07
ATOM	1278	CB	ASN	263	45.872	47.495	-13.119	1.00	36.54
ATOM	1279	CG	ASN	263	46.483	46.467	-12.141	1.00	48.06
ATOM	1280	OD1	ASN	263	47.677	46.416	-11.842	1.00	52.97
ATOM	1281	ND2	ASN	263	45.694	45.600	-11.517	1.00	50.97
ATOM	1282	HD21	ASN	263	44.728	45.639	-11.681	1.00	0.00
ATOM	1283	HD22	ASN	263	46.129	44.947	-10.928	1.00	0.00
ATOM	1284	C	ASN	263	46.450	49.332	-14.673	1.00	31.78
ATOM	1285	O	ASN	263	47.043	49.081	-15.715	1.00	30.44
ATOM	1286	N	MET	264	45.443	50.203	-14.640	1.00	30.71
ATOM	1287	H	MET	264	44.940	50.348	-13.807	1.00	0.00
ATOM	1288	CA	MET	264	45.054	50.956	-15.817	1.00	31.45
ATOM	1289	CB	MET	264	43.742	51.698	-15.565	1.00	36.38
ATOM	1290	CG	MET	264	42.352	50.779	-15.835	1.00	44.27
ATOM	1291	SD	MET	264	40.953	51.627	-15.768	1.00	51.17
ATOM	1292	CE	MET	264	40.447	51.015	-14.191	1.00	51.48
ATOM	1293	C	MET	264	46.036	51.979	-16.362	1.00	30.63
ATOM	1294	O	MET	264	45.903	52.396	-17.500	1.00	25.16
ATOM	1295	N	LEU	265	47.044	52.435	-15.617	1.00	27.60
ATOM	1296	H	LEU	265	47.167	52.116	-14.695	1.00	0.00
ATOM	1297	CA	LEU	265	47.941	53.456	-16.133	1.00	23.27
ATOM	1298	CB	LEU	265	47.844	54.709	-15.272	1.00	24.95
ATOM	1299	CG	LEU	265	46.508	55.432	-15.452	1.00	30.77
ATOM	1300	CD1	LEU	265	45.942	55.833	-14.099	1.00	35.13
ATOM	1301	CD2	LEU	265	46.722	56.641	-16.339	1.00	30.86
ATOM	1302	C	LEU	265	49.365	52.980	-16.157	1.00	21.55
ATOM	1303	O	LEU	265	50.309	53.724	-16.327	1.00	21.21
ATOM	1304	N	ASN	266	49.583	51.696	-15.972	1.00	20.49
ATOM	1305	H	ASN	266	48.832	51.117	-15.737	1.00	0.00
ATOM	1306	CA	ASN	266	50.918	51.154	-16.072	1.00	21.68
ATOM	1307	CB	ASN	266	50.905	49.810	-15.355	1.00	20.66
ATOM	1308	CG	ASN	266	50.208	48.692	-16.103	1.00	26.15
ATOM	1309	OD1	ASN	266	50.004	48.725	-17.302	1.00	30.13
ATOM	1310	ND2	ASN	266	49.889	47.599	-15.435	1.00	26.18
ATOM	1311	HD21	ASN	266	50.148	47.527	-14.492	1.00	0.00
ATOM	1312	HD22	ASN	266	49.389	46.885	-15.880	1.00	0.00
ATOM	1313	C	ASN	266	51.463	51.028	-17.496	1.00	27.52
ATOM	1314	O	ASN	266	50.834	51.391	-18.480	1.00	25.25
ATOM	1315	N	THR	267	52.671	50.496	-17.668	1.00	29.62
ATOM	1316	H	THR	267	53.155	50.095	-16.911	1.00	0.00
ATOM	1317	CA	THR	267	53.325	50.491	-18.965	1.00	31.01
ATOM	1318	CB	THR	267	54.807	50.073	-18.787	1.00	31.03
ATOM	1319	OG1	THR	267	55.330	51.030	-17.858	1.00	36.10
ATOM	1320	HG1	THR	267	54.960	50.998	-16.964	1.00	0.00
ATOM	1321	CG2	THR	267	55.686	50.139	-20.052	1.00	28.06
ATOM	1322	C	THR	267	52.618	49.591	-19.933	1.00	31.70
ATOM	1323	O	THR	267	52.606	49.803	-21.128	1.00	31.87
ATOM	1324	N	LYS	268	51.988	48.543	-19.427	1.00	34.40
ATOM	1325	H	LYS	268	52.010	48.391	-18.464	1.00	0.00
ATOM	1326	CA	LYS	268	51.228	47.643	-20.275	1.00	34.41
ATOM	1327	CB	LYS	268	50.800	46.427	-19.458	1.00	38.03
ATOM	1328	CG	LYS	268	49.912	45.417	-20.194	1.00	46.78
ATOM	1329	CD	LYS	268	49.406	44.239	-19.341	1.00	51.28
ATOM	1330	CE	LYS	268	48.410	44.674	-18.258	1.00	59.23
ATOM	1331	NZ	LYS	268	47.936	43.541	-17.483	1.00	63.39
ATOM	1332	HZ1	LYS	268	48.737	43.066	-17.022	1.00	0.00
ATOM	1333	HZ2	LYS	268	47.453	42.877	-18.122	1.00	0.00
ATOM	1334	HZ3	LYS	268	47.263	43.878	-16.766	1.00	0.00
ATOM	1335	C	LYS	268	50.013	48.367	-20.803	1.00	34.09

ATOM	1336	O	LYS	268	49.735	48.325	-21.979	1.00	34.97
ATOM	1337	N	ASN	269	49.267	49.054	-19.948	1.00	29.59
ATOM	1338	H	ASN	269	49.577	49.149	-19.020	1.00	0.00
ATOM	1339	CA	ASN	269	48.012	49.651	-20.366	1.00	24.54
ATOM	1340	CB	ASN	269	46.995	49.607	-19.263	1.00	26.50
ATOM	1341	CG	ASN	269	46.685	48.179	-19.067	1.00	32.19
ATOM	1342	OD1	ASN	269	46.295	47.488	-19.988	1.00	35.32
ATOM	1343	ND2	ASN	269	46.896	47.620	-17.892	1.00	35.76
ATOM	1344	HD21	ASN	269	47.263	48.175	-17.168	1.00	0.00
ATOM	1345	HD22	ASN	269	46.674	46.672	-17.821	1.00	0.00
ATOM	1346	C	ASN	269	48.130	51.078	-20.767	1.00	27.02
ATOM	1347	O	ASN	269	47.253	51.677	-21.370	1.00	27.85
ATOM	1348	N	CYS	270	49.228	51.744	-20.458	1.00	26.07
ATOM	1349	H	CYS	270	49.948	51.324	-19.931	1.00	0.00
ATOM	1350	CA	CYS	270	49.351	53.133	-20.848	1.00	23.70
ATOM	1351	CB	CYS	270	49.028	54.048	-19.676	1.00	22.29
ATOM	1352	SG	CYS	270	48.971	55.800	-20.133	1.00	27.75
ATOM	1353	C	CYS	270	50.770	53.374	-21.287	1.00	26.34
ATOM	1354	O	CYS	270	51.515	54.159	-20.711	1.00	24.34
ATOM	1355	N	PRO	271	51.237	52.761	-22.313	1.00	26.04
ATOM	1356	CD	PRO	271	50.428	52.006	-23.263	1.00	26.80
ATOM	1357	CA	PRO	271	52.628	52.860	-22.730	1.00	26.32
ATOM	1358	CB	PRO	271	52.694	51.997	-23.974	1.00	25.30
ATOM	1359	CG	PRO	271	51.292	52.036	-24.514	1.00	24.28
ATOM	1360	C	PRO	271	53.104	54.281	-22.955	1.00	29.26
ATOM	1361	O	PRO	271	54.259	54.644	-22.776	1.00	31.29
ATOM	1362	N	SER	272	52.220	55.180	-23.365	1.00	30.94
ATOM	1363	H	SER	272	51.287	54.942	-23.574	1.00	0.00
ATOM	1364	CA	SER	272	52.617	56.555	-23.545	1.00	31.44
ATOM	1365	CB	SER	272	51.440	57.305	-24.135	1.00	37.05
ATOM	1366	OG	SER	272	50.225	56.635	-23.790	1.00	53.17
ATOM	1367	HG	SER	272	50.053	56.659	-22.840	1.00	0.00
ATOM	1368	C	SER	272	53.068	57.208	-22.269	1.00	30.10
ATOM	1369	O	SER	272	53.666	58.259	-22.345	1.00	30.70
ATOM	1370	N	LEU	273	52.826	56.687	-21.064	1.00	29.16
ATOM	1371	H	LEU	273	52.343	55.839	-20.921	1.00	0.00
ATOM	1372	CA	LEU	273	53.350	57.384	-19.910	1.00	26.90
ATOM	1373	CB	LEU	273	52.250	57.567	-18.851	1.00	23.25
ATOM	1374	CG	LEU	273	51.343	58.788	-19.139	1.00	24.56
ATOM	1375	CD1	LEU	273	50.112	58.798	-18.225	1.00	20.80
ATOM	1376	CD2	LEU	273	52.168	60.056	-18.965	1.00	20.75
ATOM	1377	C	LEU	273	54.519	56.632	-19.336	1.00	28.09
ATOM	1378	O	LEU	273	54.948	56.803	-18.205	1.00	24.97
ATOM	1379	N	LYS	274	55.108	55.731	-20.112	1.00	28.29
ATOM	1380	H	LYS	274	54.753	55.544	-21.008	1.00	0.00
ATOM	1381	CA	LYS	274	56.314	55.053	-19.684	1.00	27.08
ATOM	1382	CB	LYS	274	56.853	54.212	-20.819	1.00	28.08
ATOM	1383	CG	LYS	274	58.111	53.417	-20.485	1.00	32.44
ATOM	1384	CD	LYS	274	58.619	52.783	-21.777	1.00	40.58
ATOM	1385	CE	LYS	274	59.960	52.073	-21.658	1.00	45.30
ATOM	1386	NZ	LYS	274	61.040	53.035	-21.669	1.00	47.25
ATOM	1387	HZ1	LYS	274	60.925	53.685	-20.867	1.00	0.00
ATOM	1388	HZ2	LYS	274	61.021	53.571	-22.560	1.00	0.00
ATOM	1389	HZ3	LYS	274	61.949	52.537	-21.580	1.00	0.00
ATOM	1390	C	LYS	274	57.348	56.087	-19.285	1.00	27.81
ATOM	1391	O	LYS	274	57.594	57.057	-19.983	1.00	27.52
ATOM	1392	N	ASP	275	57.942	55.858	-18.123	1.00	26.78
ATOM	1393	H	ASP	275	57.514	55.152	-17.599	1.00	0.00
ATOM	1394	CA	ASP	275	59.007	56.689	-17.546	1.00	24.40
ATOM	1395	CB	ASP	275	60.222	56.827	-18.507	1.00	24.70
ATOM	1396	CG	ASP	275	60.849	55.482	-18.831	1.00	28.62
ATOM	1397	OD1	ASP	275	61.282	55.358	-19.970	1.00	35.31
ATOM	1398	OD2	ASP	275	60.919	54.577	-17.980	1.00	31.34
ATOM	1399	C	ASP	275	58.618	58.090	-17.114	1.00	21.07

ATOM	1400	O	ASP	275	59.450	58.931	-16.787	1.00	22.30
ATOM	1401	N	LYS	276	57.332	58.409	-17.087	1.00	20.11
ATOM	1402	H	LYS	276	56.635	57.754	-17.318	1.00	0.00
ATOM	1403	CA	LYS	276	56.918	59.738	-16.690	1.00	20.03
ATOM	1404	CB	LYS	276	55.977	60.268	-17.772	1.00	15.62
ATOM	1405	CG	LYS	276	56.700	60.352	-19.129	1.00	20.79
ATOM	1406	CD	LYS	276	55.762	60.741	-20.275	1.00	25.10
ATOM	1407	CE	LYS	276	56.341	60.584	-21.682	1.00	24.43
ATOM	1408	NZ	LYS	276	55.317	60.858	-22.677	1.00	26.93
ATOM	1409	HZ1	LYS	276	54.962	61.828	-22.562	1.00	0.00
ATOM	1410	HZ2	LYS	276	54.528	60.192	-22.550	1.00	0.00
ATOM	1411	HZ3	LYS	276	55.716	60.744	-23.630	1.00	0.00
ATOM	1412	C	LYS	276	56.238	59.664	-15.339	1.00	21.33
ATOM	1413	O	LYS	276	55.549	58.696	-15.080	1.00	23.74
ATOM	1414	N	PRO	277	56.342	60.565	-14.432	1.00	18.25
ATOM	1415	CD	PRO	277	57.125	61.779	-14.555	1.00	20.11
ATOM	1416	CA	PRO	277	55.658	60.491	-13.158	1.00	19.61
ATOM	1417	CB	PRO	277	56.178	61.665	-12.348	1.00	19.47
ATOM	1418	CG	PRO	277	57.365	62.160	-13.113	1.00	17.30
ATOM	1419	C	PRO	277	54.146	60.506	-13.252	1.00	21.46
ATOM	1420	O	PRO	277	53.522	61.268	-13.988	1.00	24.07
ATOM	1421	N	LYS	278	53.531	59.642	-12.473	1.00	19.22
ATOM	1422	H	LYS	278	54.049	58.986	-11.955	1.00	0.00
ATOM	1423	CA	LYS	278	52.093	59.598	-12.436	1.00	18.47
ATOM	1424	CB	LYS	278	51.654	58.233	-12.953	1.00	16.94
ATOM	1425	CG	LYS	278	52.074	58.090	-14.435	1.00	15.20
ATOM	1426	CD	LYS	278	51.919	56.673	-14.945	1.00	16.03
ATOM	1427	CE	LYS	278	53.057	55.723	-14.550	1.00	18.36
ATOM	1428	NZ	LYS	278	54.258	55.975	-15.318	1.00	19.84
ATOM	1429	HZ1	LYS	278	54.573	56.952	-15.158	1.00	0.00
ATOM	1430	HZ2	LYS	278	54.052	55.841	-16.328	1.00	0.00
ATOM	1431	HZ3	LYS	278	55.008	55.317	-15.025	1.00	0.00
ATOM	1432	C	LYS	278	51.698	59.807	-11.016	1.00	21.76
ATOM	1433	O	LYS	278	51.903	58.916	-10.202	1.00	23.16
ATOM	1434	N	VAL	279	51.133	60.956	-10.655	1.00	18.92
ATOM	1435	H	VAL	279	50.893	61.619	-11.338	1.00	0.00
ATOM	1436	CA	VAL	279	50.830	61.249	-9.270	1.00	16.68
ATOM	1437	CB	VAL	279	51.262	62.707	-8.960	1.00	15.16
ATOM	1438	CG1	VAL	279	51.042	63.041	-7.484	1.00	12.89
ATOM	1439	CG2	VAL	279	52.737	62.882	-9.318	1.00	13.20
ATOM	1440	C	VAL	279	49.340	61.054	-9.066	1.00	20.13
ATOM	1441	O	VAL	279	48.520	61.647	-9.770	1.00	20.96
ATOM	1442	N	ILE	280	48.946	60.212	-8.099	1.00	20.07
ATOM	1443	H	ILE	280	49.628	59.772	-7.543	1.00	0.00
ATOM	1444	CA	ILE	280	47.535	59.939	-7.830	1.00	20.53
ATOM	1445	CB	ILE	280	47.306	58.401	-7.914	1.00	25.21
ATOM	1446	CG2	ILE	280	45.900	58.000	-7.454	1.00	17.77
ATOM	1447	CG1	ILE	280	47.519	57.977	-9.377	1.00	24.13
ATOM	1448	CD1	ILE	280	48.045	56.562	-9.513	1.00	30.13
ATOM	1449	C	ILE	280	47.150	60.496	-6.467	1.00	21.62
ATOM	1450	O	ILE	280	47.789	60.204	-5.464	1.00	22.51
ATOM	1451	N	ILE	281	46.108	61.318	-6.363	1.00	20.14
ATOM	1452	H	ILE	281	45.542	61.495	-7.148	1.00	0.00
ATOM	1453	CA	ILE	281	45.770	61.940	-5.109	1.00	19.43
ATOM	1454	CB	ILE	281	45.858	63.465	-5.300	1.00	19.82
ATOM	1455	CG2	ILE	281	45.338	64.229	-4.081	1.00	16.34
ATOM	1456	CG1	ILE	281	47.333	63.810	-5.516	1.00	24.03
ATOM	1457	CD1	ILE	281	47.627	65.269	-5.781	1.00	26.46
ATOM	1458	C	ILE	281	44.389	61.476	-4.737	1.00	22.29
ATOM	1459	O	ILE	281	43.495	61.498	-5.568	1.00	21.67
ATOM	1460	N	ILE	282	44.128	61.032	-3.509	1.00	23.39
ATOM	1461	H	ILE	282	44.833	61.012	-2.823	1.00	0.00
ATOM	1462	CA	ILE	282	42.781	60.593	-3.163	1.00	24.32
ATOM	1463	CB	ILE	282	42.761	59.050	-3.045	1.00	21.45

ATOM	1464	CG2	ILE	282	41.368	58.517	-2.706	1.00	22.39
ATOM	1465	CG1	ILE	282	43.224	58.492	-4.387	1.00	17.29
ATOM	1466	CD1	ILE	282	43.645	57.044	-4.387	1.00	18.62
ATOM	1467	C	ILE	282	42.275	61.214	-1.878	1.00	24.17
ATOM	1468	O	ILE	282	42.837	61.022	-0.802	1.00	23.02
ATOM	1469	N	GLN	283	41.195	61.985	-1.981	1.00	24.17
ATOM	1470	H	GLN	283	40.880	62.229	-2.879	1.00	0.00
ATOM	1471	CA	GLN	283	40.417	62.361	-0.807	1.00	26.94
ATOM	1472	CB	GLN	283	39.916	63.809	-0.951	1.00	29.78
ATOM	1473	CG	GLN	283	38.790	64.295	-0.003	1.00	30.76
ATOM	1474	CD	GLN	283	39.213	64.338	1.454	1.00	31.96
ATOM	1475	OE1	GLN	283	40.263	64.820	1.835	1.00	26.84
ATOM	1476	NE2	GLN	283	38.367	63.923	2.370	1.00	32.78
ATOM	1477	HE21	GLN	283	37.468	63.628	2.058	1.00	0.00
ATOM	1478	HE22	GLN	283	38.632	63.911	3.299	1.00	0.00
ATOM	1479	C	GLN	283	39.227	61.397	-0.673	1.00	27.75
ATOM	1480	O	GLN	283	38.396	61.282	-1.580	1.00	27.45
ATOM	1481	N	ALA	284	39.127	60.692	0.460	1.00	24.57
ATOM	1482	H	ALA	284	39.827	60.742	1.148	1.00	0.00
ATOM	1483	CA	ALA	284	38.115	59.682	0.688	1.00	22.92
ATOM	1484	CB	ALA	284	38.196	58.595	-0.383	1.00	15.36
ATOM	1485	C	ALA	284	38.438	59.060	2.029	1.00	25.81
ATOM	1486	O	ALA	284	39.598	58.871	2.387	1.00	29.97
ATOM	1487	N	ALD	285	37.396	58.754	2.795	1.00	27.43
ATOM	1488	CA	ALD	285	37.538	58.081	4.104	1.00	26.59
ATOM	1489	C	ALD	285	38.038	56.689	3.860	1.00	26.61
ATOM	1490	O	ALD	285	37.779	56.155	2.790	1.00	30.02
ATOM	1491	CB	ALD	285	36.215	57.908	4.846	1.00	26.43
ATOM	1492	SG	ALD	285	35.603	59.475	5.487	1.00	34.69
ATOM	1493	N1	ALD	285	32.516	69.905	10.851	1.00	58.66
ATOM	1494	C1	ALD	285	33.306	68.911	10.160	1.00	48.23
ATOM	1495	C5	ALD	285	32.529	67.649	10.069	1.00	45.89
ATOM	1496	O2	ALD	285	31.833	67.247	10.983	1.00	47.20
ATOM	1497	C9	ALD	285	34.623	68.691	10.902	1.00	46.18
ATOM	1498	CG	ALD	285	35.549	69.731	10.350	1.00	50.40
ATOM	1499	CD1	ALD	285	35.586	71.002	10.923	1.00	53.28
ATOM	1500	CD2	ALD	285	36.268	69.456	9.185	1.00	53.34
ATOM	1501	CE1	ALD	285	36.376	71.984	10.326	1.00	55.15
ATOM	1502	CE2	ALD	285	37.056	70.446	8.595	1.00	52.67
ATOM	1503	CZ	ALD	285	37.109	71.725	9.163	1.00	57.31
ATOM	1504	OH	ALD	285	37.756	72.792	8.546	1.00	63.58
ATOM	1505	N2	ALD	285	32.657	67.034	8.925	1.00	38.70
ATOM	1506	C2	ALD	285	31.932	65.809	8.702	1.00	34.11
ATOM	1507	C6	ALD	285	33.033	64.915	8.206	1.00	33.25
ATOM	1508	O3	ALD	285	34.021	65.383	7.657	1.00	27.84
ATOM	1509	C10	ALD	285	30.819	66.116	7.661	1.00	39.67
ATOM	1510	CG1	ALD	285	30.399	64.915	6.822	1.00	44.49
ATOM	1511	CG2	ALD	285	29.588	66.547	8.453	1.00	40.46
ATOM	1512	N3	ALD	285	32.851	63.630	8.422	1.00	31.01
ATOM	1513	C3	ALD	285	33.824	62.646	7.997	1.00	33.50
ATOM	1514	C7	ALD	285	33.316	62.147	6.681	1.00	37.64
ATOM	1515	O4	ALD	285	32.114	62.219	6.432	1.00	44.05
ATOM	1516	C11	ALD	285	33.899	61.464	8.952	1.00	31.45
ATOM	1517	N4	ALD	285	34.265	61.650	5.908	1.00	35.48
ATOM	1518	C4	ALD	285	34.210	61.553	4.464	1.00	33.98
ATOM	1519	C8	ALD	285	34.763	60.203	4.008	1.00	36.52
ATOM	1520	C12	ALD	285	35.030	62.710	3.971	1.00	35.04
ATOM	1521	C13	ALD	285	34.835	62.936	2.510	1.00	37.05
ATOM	1522	OD1	ALD	285	35.766	63.453	1.898	1.00	37.30
ATOM	1523	OD2	ALD	285	33.772	62.594	1.993	1.00	34.87
ATOM	1524	O5	ALD	285	33.751	59.337	3.478	1.00	42.82
ATOM	1525	H1	ALD	285	36.497	58.977	2.418	1.00	0.00
ATOM	1526	C14	ALD	285	31.983	70.803	10.042	1.00	65.26
ATOM	1527	H5	ALD	285	32.384	69.885	11.844	1.00	0.00

ATOM	1528	H6	ALD	285	37.739	72.711	7.587	1.00	0.00
ATOM	1529	H7	ALD	285	33.249	67.364	8.179	1.00	0.00
ATOM	1530	H8	ALD	285	32.004	63.310	8.842	1.00	0.00
ATOM	1531	H9	ALD	285	35.098	61.322	6.347	1.00	0.00
ATOM	1532	C15	ALD	285	30.476	70.799	10.002	1.00	65.03
ATOM	1533	O1	ALD	285	32.684	71.569	9.386	1.00	73.24
ATOM	1534	H2	ALD	285	35.481	60.411	3.215	1.00	0.00
ATOM	1535	N	ARG	286	38.740	56.061	4.793	1.00	26.38
ATOM	1536	H	ARG	286	38.960	56.493	5.651	1.00	0.00
ATOM	1537	CA	ARG	286	39.231	54.719	4.550	1.00	25.85
ATOM	1538	CB	ARG	286	40.747	54.692	4.682	1.00	24.02
ATOM	1539	CG	ARG	286	41.387	55.701	3.739	1.00	23.75
ATOM	1540	CD	ARG	286	42.430	54.961	2.926	1.00	27.07
ATOM	1541	NE	ARG	286	43.768	55.251	3.356	1.00	29.64
ATOM	1542	HE	ARG	286	43.926	55.944	4.031	1.00	0.00
ATOM	1543	CZ	ARG	286	44.798	54.588	2.845	1.00	26.29
ATOM	1544	NH1	ARG	286	46.050	55.018	3.144	1.00	25.89
ATOM	1545	HH11	ARG	286	46.181	55.814	3.735	1.00	0.00
ATOM	1546	HH12	ARG	286	46.845	54.538	2.774	1.00	0.00
ATOM	1547	NH2	ARG	286	44.621	53.491	2.058	1.00	19.53
ATOM	1548	HH21	ARG	286	43.700	53.161	1.851	1.00	0.00
ATOM	1549	HH22	ARG	286	45.416	53.010	1.689	1.00	0.00
ATOM	1550	C	ARG	286	38.629	53.755	5.538	1.00	26.43
ATOM	1551	O	ARG	286	39.160	52.683	5.803	1.00	27.12
ATOM	1552	N	GLY	287	37.495	54.113	6.133	1.00	26.73
ATOM	1553	H	GLY	287	37.021	54.925	5.843	1.00	0.00
ATOM	1554	CA	GLY	287	36.905	53.350	7.208	1.00	27.46
ATOM	1555	C	GLY	287	36.162	54.330	8.100	1.00	30.03
ATOM	1556	O	GLY	287	35.932	55.475	7.728	1.00	32.06
ATOM	1557	N	ASP	288	35.804	53.848	9.292	1.00	33.55
ATOM	1558	H	ASP	288	36.263	53.019	9.545	1.00	0.00
ATOM	1559	CA	ASP	288	34.941	54.525	10.273	1.00	32.84
ATOM	1560	CB	ASP	288	33.839	53.609	10.820	1.00	40.57
ATOM	1561	CG	ASP	288	33.043	52.985	9.706	1.00	48.86
ATOM	1562	OD1	ASP	288	33.051	51.752	9.612	1.00	53.99
ATOM	1563	OD2	ASP	288	32.413	53.731	8.944	1.00	51.26
ATOM	1564	C	ASP	288	35.710	55.003	11.500	1.00	31.98
ATOM	1565	O	ASP	288	35.283	55.884	12.250	1.00	32.42
ATOM	1566	N	SER	289	36.884	54.437	11.775	1.00	28.78
ATOM	1567	H	SER	289	37.321	53.757	11.200	1.00	0.00
ATOM	1568	CA	SER	289	37.596	54.805	12.969	1.00	24.44
ATOM	1569	CB	SER	289	38.704	53.801	13.071	1.00	22.45
ATOM	1570	OG	SER	289	38.083	52.535	13.042	1.00	33.26
ATOM	1571	HG	SER	289	38.773	51.861	13.003	1.00	0.00
ATOM	1572	C	SER	289	38.069	56.239	12.940	1.00	24.99
ATOM	1573	O	SER	289	38.394	56.809	11.907	1.00	26.10
ATOM	1574	N	PRO	290	38.143	56.885	14.041	1.00	27.20
ATOM	1575	CD	PRO	290	37.408	56.497	15.249	1.00	22.52
ATOM	1576	CA	PRO	290	38.631	58.270	14.136	1.00	25.66
ATOM	1577	CB	PRO	290	38.051	58.769	15.454	1.00	27.04
ATOM	1578	CG	PRO	290	37.920	57.494	16.266	1.00	21.06
ATOM	1579	C	PRO	290	40.138	58.521	14.026	1.00	28.40
ATOM	1580	O	PRO	290	40.637	59.638	13.939	1.00	26.84
ATOM	1581	N	GLY	291	40.904	57.441	14.034	1.00	24.70
ATOM	1582	H	GLY	291	40.473	56.576	14.160	1.00	0.00
ATOM	1583	CA	GLY	291	42.342	57.513	13.835	1.00	27.48
ATOM	1584	C	GLY	291	43.153	57.845	15.056	1.00	26.97
ATOM	1585	O	GLY	291	44.292	58.236	14.877	1.00	24.56
ATOM	1586	N	VAL	292	42.646	57.715	16.287	1.00	24.36
ATOM	1587	H	VAL	292	41.794	57.243	16.414	1.00	0.00
ATOM	1588	CA	VAL	292	43.348	58.171	17.491	1.00	26.77
ATOM	1589	CB	VAL	292	42.800	59.510	18.102	1.00	24.74
ATOM	1590	CG1	VAL	292	43.027	60.664	17.151	1.00	28.54
ATOM	1591	CG2	VAL	292	41.311	59.404	18.371	1.00	25.92

ATOM	1592	C	VAL	292	43.273	57.168	18.641	1.00	26.43
ATOM	1593	O	VAL	292	42.441	56.276	18.749	1.00	28.53
ATOM	1594	N	VAL	293	44.199	57.326	19.569	1.00	27.36
ATOM	1595	H	VAL	293	44.833	58.079	19.525	1.00	0.00
ATOM	1596	CA	VAL	293	44.287	56.466	20.719	1.00	28.84
ATOM	1597	CB	VAL	293	45.426	55.456	20.369	1.00	27.36
ATOM	1598	CG1	VAL	293	46.801	55.914	20.801	1.00	23.55
ATOM	1599	CG2	VAL	293	45.069	54.152	21.025	1.00	28.81
ATOM	1600	C	VAL	293	44.564	57.485	21.845	1.00	30.19
ATOM	1601	O	VAL	293	45.149	58.538	21.595	1.00	30.10
ATOM	1602	N	TRP	294	44.153	57.245	23.098	1.00	27.38
ATOM	1603	H	TRP	294	43.657	56.424	23.290	1.00	0.00
ATOM	1604	CA	TRP	294	44.490	58.156	24.193	1.00	26.27
ATOM	1605	CB	TRP	294	43.553	58.075	25.389	1.00	24.27
ATOM	1606	CG	TRP	294	42.160	58.474	25.030	1.00	26.12
ATOM	1607	CD2	TRP	294	41.796	59.897	24.914	1.00	27.34
ATOM	1608	CE2	TRP	294	40.345	59.680	24.556	1.00	25.56
ATOM	1609	CE3	TRP	294	42.296	61.171	25.019	1.00	28.09
ATOM	1610	CD1	TRP	294	41.128	57.603	24.792	1.00	25.19
ATOM	1611	NE1	TRP	294	40.077	58.356	24.518	1.00	28.67
ATOM	1612	HE1	TRP	294	39.189	57.990	24.324	1.00	0.00
ATOM	1613	CZ2	TRP	294	39.526	60.761	24.347	1.00	21.74
ATOM	1614	CZ3	TRP	294	41.421	62.218	24.795	1.00	27.80
ATOM	1615	CH2	TRP	294	40.084	62.017	24.478	1.00	25.43
ATOM	1616	C	TRP	294	45.823	57.790	24.766	1.00	27.42
ATOM	1617	O	TRP	294	46.217	56.632	24.801	1.00	26.36
ATOM	1618	N	PHE	295	46.574	58.751	25.251	1.00	32.18
ATOM	1619	H	PHE	295	46.375	59.702	25.116	1.00	0.00
ATOM	1620	CA	PHE	295	47.704	58.370	26.063	1.00	41.42
ATOM	1621	CB	PHE	295	49.007	58.377	25.207	1.00	40.27
ATOM	1622	CG	PHE	295	49.439	59.770	24.852	1.00	44.54
ATOM	1623	CD1	PHE	295	50.325	60.433	25.679	1.00	45.58
ATOM	1624	CD2	PHE	295	48.853	60.419	23.779	1.00	48.03
ATOM	1625	CE1	PHE	295	50.559	61.777	25.480	1.00	49.71
ATOM	1626	CE2	PHE	295	49.086	61.764	23.583	1.00	47.03
ATOM	1627	CZ	PHE	295	49.928	62.441	24.444	1.00	52.74
ATOM	1628	C	PHE	295	47.765	59.359	27.208	1.00	46.22
ATOM	1629	O	PHE	295	47.343	60.503	27.145	1.00	42.87
ATOM	1630	N	LYS	296	48.314	58.905	28.316	1.00	57.30
ATOM	1631	H	LYS	296	48.708	58.012	28.341	1.00	0.00
ATOM	1632	CA	LYS	296	48.421	59.737	29.496	1.00	64.18
ATOM	1633	CB	LYS	296	48.497	58.862	30.739	1.00	65.20
ATOM	1634	CG	LYS	296	48.184	59.668	31.988	1.00	68.41
ATOM	1635	CD	LYS	296	47.966	58.760	33.189	1.00	72.60
ATOM	1636	CE	LYS	296	49.201	57.947	33.534	1.00	75.23
ATOM	1637	NZ	LYS	296	50.320	58.836	33.780	1.00	81.49
ATOM	1638	HZ	LYS	296	50.088	59.472	34.569	1.00	0.00
ATOM	1639	HZ2	LYS	296	50.511	59.398	32.925	1.00	0.00
ATOM	1640	HZ3	LYS	296	51.159	58.270	34.015	1.00	0.00
ATOM	1641	C	LYS	296	49.684	60.547	29.397	1.00	68.26
ATOM	1642	O	LYS	296	50.729	59.951	29.161	1.00	72.09
ATOM	1643	N	ASP	297	49.591	61.860	29.569	1.00	72.66
ATOM	1644	H	ASP	297	49.170	62.489	28.934	1.00	0.00
ATOM	1645	CA	ASP	297	50.160	62.460	30.750	1.00	82.26
ATOM	1646	CB	ASP	297	51.698	62.430	30.748	1.00	88.06
ATOM	1647	CG	ASP	297	52.196	61.867	32.082	1.00	92.95
ATOM	1648	OD1	ASP	297	51.766	62.345	33.140	1.00	94.73
ATOM	1649	OD2	ASP	297	53.019	60.945	32.067	1.00	96.27
ATOM	1650	C	ASP	297	49.705	63.893	30.706	1.00	84.91
ATOM	1651	O	ASP	297	49.463	64.419	29.608	1.00	87.39
ATOM	1652	OT	ASP	297	49.571	64.477	31.777	1.00	84.32
ATOM	1653	CB	ALA	317	65.517	45.642	-31.211	1.00	60.98
ATOM	1654	C	ALA	317	63.053	45.718	-30.743	1.00	55.95
ATOM	1655	O	ALA	317	62.644	46.858	-30.593	1.00	55.33

ATOM	1656	HT1	ALA	317	63.898	47.390	-32.203	1.00	0.00
ATOM	1657	HT2	ALA	317	62.879	46.419	-33.062	1.00	0.00
ATOM	1658	N	ALA	317	63.865	46.499	-32.753	1.00	63.55
ATOM	1659	HT3	ALA	317	64.541	46.464	-33.540	1.00	0.00
ATOM	1660	CA	ALA	317	64.124	45.449	-31.790	1.00	59.35
ATOM	1661	N	ILE	318	62.584	44.702	-30.035	1.00	52.67
ATOM	1662	H	ILE	318	62.850	43.777	-30.235	1.00	0.00
ATOM	1663	CA	ILE	318	61.755	44.926	-28.863	1.00	48.35
ATOM	1664	CB	ILE	318	60.789	43.749	-28.729	1.00	43.28
ATOM	1665	CG2	ILE	318	59.718	43.915	-29.796	1.00	39.84
ATOM	1666	CG1	ILE	318	61.523	42.407	-28.849	1.00	35.21
ATOM	1667	CD1	ILE	318	60.596	41.194	-28.946	1.00	36.89
ATOM	1668	C	ILE	318	62.702	45.020	-27.656	1.00	48.70
ATOM	1669	O	ILE	318	63.754	44.390	-27.651	1.00	46.83
ATOM	1670	N	LYS	319	62.351	45.808	-26.630	1.00	47.06
ATOM	1671	H	LYS	319	61.527	46.341	-26.691	1.00	0.00
ATOM	1672	CA	LYS	319	63.102	45.893	-25.383	1.00	42.30
ATOM	1673	CB	LYS	319	63.641	47.280	-25.184	1.00	46.07
ATOM	1674	CG	LYS	319	65.100	47.492	-25.528	1.00	59.38
ATOM	1675	CD	LYS	319	65.488	48.878	-24.982	1.00	73.60
ATOM	1676	CE	LYS	319	66.995	49.115	-24.757	1.00	83.83
ATOM	1677	NZ	LYS	319	67.263	50.131	-23.739	1.00	85.82
ATOM	1678	HZ1	LYS	319	66.878	49.820	-22.825	1.00	0.00
ATOM	1679	HZ2	LYS	319	66.840	51.037	-24.022	1.00	0.00
ATOM	1680	HZ3	LYS	319	68.294	50.246	-23.654	1.00	0.00
ATOM	1681	C	LYS	319	62.157	45.597	-24.229	1.00	36.54
ATOM	1682	O	LYS	319	60.960	45.806	-24.324	1.00	36.02
ATOM	1683	N	LYS	320	62.635	45.096	-23.105	1.00	34.11
ATOM	1684	H	LYS	320	63.577	44.830	-23.064	1.00	0.00
ATOM	1685	CA	LYS	320	61.823	44.993	-21.894	1.00	35.41
ATOM	1686	CB	LYS	320	62.389	43.928	-20.978	1.00	36.15
ATOM	1687	CG	LYS	320	62.391	42.526	-21.549	1.00	40.56
ATOM	1688	CD	LYS	320	63.120	41.594	-20.583	1.00	40.42
ATOM	1689	CE	LYS	320	63.108	40.150	-21.065	1.00	43.28
ATOM	1690	NZ	LYS	320	64.002	39.368	-20.235	1.00	52.04
ATOM	1691	HZ1	LYS	320	63.689	39.403	-19.245	1.00	0.00
ATOM	1692	HZ2	LYS	320	64.966	39.751	-20.319	1.00	0.00
ATOM	1693	HZ3	LYS	320	63.995	38.382	-20.571	1.00	0.00
ATOM	1694	C	LYS	320	61.701	46.280	-21.053	1.00	33.67
ATOM	1695	O	LYS	320	62.635	47.066	-20.917	1.00	31.28
ATOM	1696	N	ALA	321	60.521	46.503	-20.461	1.00	28.86
ATOM	1697	H	ALA	321	59.777	45.870	-20.580	1.00	0.00
ATOM	1698	CA	ALA	321	60.307	47.641	-19.592	1.00	26.84
ATOM	1699	CB	ALA	321	59.387	48.636	-20.288	1.00	26.05
ATOM	1700	C	ALA	321	59.653	47.109	-18.320	1.00	25.85
ATOM	1701	O	ALA	321	58.914	46.143	-18.310	1.00	29.15
ATOM	1702	N	HIS	322	59.889	47.690	-17.150	1.00	25.43
ATOM	1703	H	HIS	322	60.599	48.347	-17.216	1.00	0.00
ATOM	1704	CA	HIS	322	59.185	47.349	-15.904	1.00	20.62
ATOM	1705	CB	HIS	322	59.573	48.206	-14.672	1.00	18.17
ATOM	1706	CG	HIS	322	61.001	48.032	-14.197	1.00	16.95
ATOM	1707	CD2	HIS	322	61.504	46.919	-13.586	1.00	13.40
ATOM	1708	ND1	HIS	322	62.036	48.845	-14.409	1.00	20.74
ATOM	1709	HD1	HIS	322	61.980	49.784	-14.696	1.00	0.00
ATOM	1710	CE1	HIS	322	63.132	48.250	-14.001	1.00	17.22
ATOM	1711	NE2	HIS	322	62.800	47.082	-13.515	1.00	19.50
ATOM	1712	HE2	HIS	322	63.431	46.421	-13.150	1.00	0.00
ATOM	1713	C	HIS	322	57.741	47.676	-16.169	1.00	23.43
ATOM	1714	O	HIS	322	57.445	48.725	-16.715	1.00	21.27
ATOM	1715	N	ILE	323	56.837	46.786	-15.797	1.00	27.07
ATOM	1716	H	ILE	323	57.138	45.908	-15.473	1.00	0.00
ATOM	1717	CA	ILE	323	55.418	47.059	-15.946	1.00	25.91
ATOM	1718	CB	ILE	323	54.711	45.714	-15.710	1.00	23.73
ATOM	1719	CG2	ILE	323	54.531	45.378	-14.233	1.00	19.80

ATOM	1720	CG1	ILE	323	53.411	45.795	-16.461	1.00	17.37
ATOM	1721	CD1	ILE	323	52.688	44.478	-16.349	1.00	24.35
ATOM	1722	C	ILE	323	54.891	48.183	-15.046	1.00	27.83
ATOM	1723	O	ILE	323	53.998	48.930	-15.420	1.00	26.39
ATOM	1724	N	GLU	324	55.418	48.357	-13.843	1.00	27.46
ATOM	1725	H	GLU	324	56.140	47.768	-13.556	1.00	0.00
ATOM	1726	CA	GLU	324	54.973	49.441	-12.974	1.00	26.27
ATOM	1727	CB	GLU	324	54.186	48.824	-11.821	1.00	25.82
ATOM	1728	CG	GLU	324	53.692	49.837	-10.816	1.00	23.38
ATOM	1729	CD	GLU	324	52.881	49.122	-9.775	1.00	24.43
ATOM	1730	OE1	GLU	324	52.275	48.099	-10.071	1.00	25.59
ATOM	1731	OE2	GLU	324	52.858	49.586	-8.649	1.00	25.24
ATOM	1732	C	GLU	324	56.191	50.205	-12.459	1.00	29.36
ATOM	1733	O	GLU	324	57.106	49.587	-11.922	1.00	26.17
ATOM	1734	N	LYS	325	56.245	51.531	-12.604	1.00	26.30
ATOM	1735	H	LYS	325	55.526	52.005	-13.083	1.00	0.00
ATOM	1736	CA	LYS	325	57.371	52.335	-12.203	1.00	24.24
ATOM	1737	CB	LYS	325	58.571	52.036	-13.135	1.00	19.60
ATOM	1738	CG	LYS	325	59.855	52.715	-12.663	1.00	14.81
ATOM	1739	CD	LYS	325	61.087	52.259	-13.405	1.00	11.93
ATOM	1740	CE	LYS	325	61.101	52.703	-14.851	1.00	20.28
ATOM	1741	NZ	LYS	325	61.146	54.143	-14.983	1.00	21.10
ATOM	1742	HZ1	LYS	325	62.010	54.507	-14.531	1.00	0.00
ATOM	1743	HZ2	LYS	325	60.311	54.557	-14.522	1.00	0.00
ATOM	1744	HZ3	LYS	325	61.145	54.397	-15.993	1.00	0.00
ATOM	1745	C	LYS	325	56.861	53.774	-12.340	1.00	26.70
ATOM	1746	O	LYS	325	55.928	54.033	-13.094	1.00	25.97
ATOM	1747	N	ASP	326	57.480	54.700	-11.589	1.00	26.25
ATOM	1748	H	ASP	326	58.191	54.415	-10.974	1.00	0.00
ATOM	1749	CA	ASP	326	57.214	56.136	-11.610	1.00	23.30
ATOM	1750	CB	ASP	326	57.422	56.737	-13.034	1.00	23.42
ATOM	1751	CG	ASP	326	58.721	56.273	-13.707	1.00	24.74
ATOM	1752	OD1	ASP	326	59.806	56.575	-13.224	1.00	24.42
ATOM	1753	OD2	ASP	326	58.646	55.579	-14.711	1.00	21.44
ATOM	1754	C	ASP	326	55.835	56.529	-11.122	1.00	20.53
ATOM	1755	O	ASP	326	55.284	57.559	-11.488	1.00	24.45
ATOM	1756	N	PHE	327	55.222	55.721	-10.264	1.00	19.21
ATOM	1757	H	PHE	327	55.626	54.862	-10.024	1.00	0.00
ATOM	1758	CA	PHE	327	53.972	56.107	-9.608	1.00	18.83
ATOM	1759	CB	PHE	327	53.008	54.938	-9.410	1.00	16.54
ATOM	1760	CG	PHE	327	52.290	54.444	-10.658	1.00	20.45
ATOM	1761	CD1	PHE	327	51.070	55.004	-11.016	1.00	17.51
ATOM	1762	CD2	PHE	327	52.772	53.338	-11.361	1.00	21.65
ATOM	1763	CE1	PHE	327	50.334	54.424	-12.043	1.00	20.17
ATOM	1764	CE2	PHE	327	52.022	52.752	-12.380	1.00	18.97
ATOM	1765	CZ	PHE	327	50.801	53.298	-12.718	1.00	20.53
ATOM	1766	C	PHE	327	54.219	56.643	-8.201	1.00	18.93
ATOM	1767	O	PHE	327	55.237	56.323	-7.588	1.00	17.66
ATOM	1768	N	ILE	328	53.302	57.460	-7.673	1.00	18.15
ATOM	1769	H	ILE	328	52.602	57.853	-8.243	1.00	0.00
ATOM	1770	CA	ILE	328	53.255	57.771	-6.266	1.00	16.96
ATOM	1771	CB	ILE	328	54.123	59.032	-5.914	1.00	17.42
ATOM	1772	CG2	ILE	328	53.663	60.311	-6.612	1.00	19.49
ATOM	1773	CG1	ILE	328	54.026	59.244	-4.395	1.00	15.51
ATOM	1774	CD1	ILE	328	55.177	60.055	-3.780	1.00	15.10
ATOM	1775	C	ILE	328	51.802	58.030	-5.976	1.00	18.38
ATOM	1776	O	ILE	328	51.153	58.692	-6.769	1.00	18.62
ATOM	1777	N	ALA	329	51.225	57.543	-4.873	1.00	20.05
ATOM	1778	H	ALA	329	51.716	56.924	-4.289	1.00	0.00
ATOM	1779	CA	ALA	329	49.867	57.908	-4.507	1.00	20.56
ATOM	1780	CB	ALA	329	48.985	56.671	-4.395	1.00	17.55
ATOM	1781	C	ALA	329	49.854	58.614	-3.168	1.00	24.14
ATOM	1782	O	ALA	329	50.648	58.289	-2.296	1.00	22.82
ATOM	1783	N	PHE	330	48.969	59.584	-2.967	1.00	22.84

ATOM	1784	H	PHE	330	48.352	59.823	-3.694	1.00	0.00
ATOM	1785	CA	PHE	330	48.869	60.291	-1.709	1.00	18.35
ATOM	1786	CB	PHE	330	49.268	61.745	-1.937	1.00	18.09
ATOM	1787	CG	PHE	330	49.659	62.459	-0.647	1.00	22.46
ATOM	1788	CD1	PHE	330	49.771	63.841	-0.652	1.00	21.17
ATOM	1789	CD2	PHE	330	49.931	61.760	0.521	1.00	20.68
ATOM	1790	CE1	PHE	330	50.147	64.514	0.490	1.00	22.56
ATOM	1791	CE2	PHE	330	50.309	62.438	1.665	1.00	20.88
ATOM	1792	CZ	PHE	330	50.409	63.815	1.653	1.00	23.44
ATOM	1793	C	PHE	330	47.425	60.183	-1.260	1.00	20.07
ATOM	1794	O	PHE	330	46.536	60.673	-1.956	1.00	16.75
ATOM	1795	N	CYS	331	47.169	59.539	-0.117	1.00	20.04
ATOM	1796	H	CYS	331	47.914	59.170	0.402	1.00	0.00
ATOM	1797	CA	CYS	331	45.831	59.362	0.402	1.00	17.86
ATOM	1798	CB	CYS	331	45.584	57.950	0.841	1.00	16.56
ATOM	1799	SG	CYS	331	45.613	56.747	-0.490	1.00	23.49
ATOM	1800	C	CYS	331	45.649	60.235	1.609	1.00	21.19
ATOM	1801	O	CYS	331	46.586	60.508	2.342	1.00	20.65
ATOM	1802	N	SER	332	44.421	60.692	1.836	1.00	22.22
ATOM	1803	H	SER	332	43.659	60.414	1.268	1.00	0.00
ATOM	1804	CA	SER	332	44.084	61.598	2.928	1.00	21.44
ATOM	1805	CB	SER	332	42.690	62.162	2.616	1.00	19.68
ATOM	1806	OG	SER	332	41.835	61.127	2.164	1.00	24.42
ATOM	1807	HG	SER	332	40.977	61.499	2.030	1.00	0.00
ATOM	1808	C	SER	332	44.120	61.144	4.389	1.00	21.99
ATOM	1809	O	SER	332	44.290	61.947	5.302	1.00	20.58
ATOM	1810	N	SER	333	43.945	59.844	4.657	1.00	23.27
ATOM	1811	H	SER	333	43.779	59.215	3.918	1.00	0.00
ATOM	1812	CA	SER	333	43.971	59.274	5.984	1.00	20.50
ATOM	1813	CB	SER	333	42.580	58.895	6.523	1.00	21.15
ATOM	1814	OG	SER	333	41.566	58.641	5.556	1.00	23.77
ATOM	1815	HG	SER	333	40.748	58.468	6.021	1.00	0.00
ATOM	1816	C	SER	333	44.745	57.979	5.819	1.00	23.49
ATOM	1817	O	SER	333	45.104	57.510	4.736	1.00	19.23
ATOM	1818	N	THR	334	45.003	57.359	6.951	1.00	23.40
ATOM	1819	H	THR	334	44.646	57.711	7.788	1.00	0.00
ATOM	1820	CA	THR	334	45.720	56.099	6.997	1.00	24.09
ATOM	1821	CB	THR	334	46.501	56.407	8.296	1.00	28.30
ATOM	1822	OG1	THR	334	47.797	55.855	8.169	1.00	34.11
ATOM	1823	HG1	THR	334	48.191	56.183	7.351	1.00	0.00
ATOM	1824	CG2	THR	334	45.753	55.956	9.519	1.00	14.09
ATOM	1825	C	THR	334	44.639	54.990	6.904	1.00	22.20
ATOM	1826	O	THR	334	43.459	55.273	7.098	1.00	23.69
ATOM	1827	N	PRO	335	44.853	53.756	6.619	1.00	20.97
ATOM	1828	CD	PRO	335	46.175	53.207	6.414	1.00	15.82
ATOM	1829	CA	PRO	335	43.804	52.736	6.469	1.00	19.65
ATOM	1830	CB	PRO	335	44.565	51.473	6.155	1.00	20.20
ATOM	1831	CG	PRO	335	45.823	52.030	5.529	1.00	20.66
ATOM	1832	C	PRO	335	42.850	52.545	7.636	1.00	25.53
ATOM	1833	O	PRO	335	43.309	52.608	8.769	1.00	29.15
ATOM	1834	N	ASP	336	41.545	52.314	7.406	1.00	24.20
ATOM	1835	H	ASP	336	41.220	52.278	6.479	1.00	0.00
ATOM	1836	CA	ASP	336	40.529	52.137	8.449	1.00	28.39
ATOM	1837	CB	ASP	336	40.940	51.344	9.710	1.00	32.12
ATOM	1838	CG	ASP	336	41.344	49.933	9.397	1.00	43.11
ATOM	1839	OD1	ASP	336	42.285	49.465	10.040	1.00	52.99
ATOM	1840	OD2	ASP	336	40.725	49.302	8.531	1.00	51.49
ATOM	1841	C	ASP	336	40.046	53.423	9.046	1.00	29.38
ATOM	1842	O	ASP	336	39.121	53.427	9.849	1.00	34.19
ATOM	1843	N	ASN	337	40.623	54.569	8.686	1.00	25.69
ATOM	1844	H	ASN	337	41.271	54.602	7.951	1.00	0.00
ATOM	1845	CA	ASN	337	40.284	55.789	9.372	1.00	23.68
ATOM	1846	CB	ASN	337	41.565	56.352	9.973	1.00	22.73
ATOM	1847	CG	ASN	337	42.065	55.421	11.068	1.00	22.82

ATOM	1848	OD1	ASN	337	41.379	54.991	11.937	1.00	25.91
ATOM	1849	ND2	ASN	337	43.293	54.940	10.989	1.00	18.06
ATOM	1850	HD21	ASN	337	43.822	55.204	10.218	1.00	0.00
ATOM	1851	HD22	ASN	337	43.604	54.320	11.691	1.00	0.00
ATOM	1852	C	ASN	337	39.600	56.812	8.496	1.00	25.85
ATOM	1853	O	ASN	337	39.737	56.860	7.283	1.00	29.96
ATOM	1854	N	VAL	338	38.815	57.691	9.095	1.00	27.31
ATOM	1855	H	VAL	338	38.760	57.662	10.072	1.00	0.00
ATOM	1856	CA	VAL	338	38.117	58.722	8.361	1.00	24.45
ATOM	1857	CB	VAL	338	36.902	59.297	9.168	1.00	24.69
ATOM	1858	CG1	VAL	338	35.901	58.187	9.486	1.00	25.15
ATOM	1859	CG2	VAL	338	37.369	59.946	10.467	1.00	25.43
ATOM	1860	C	VAL	338	39.045	59.870	8.024	1.00	25.97
ATOM	1861	O	VAL	338	40.124	60.040	8.588	1.00	26.18
ATOM	1862	N	SER	339	38.588	60.680	7.067	1.00	27.49
ATOM	1863	H	SER	339	37.756	60.450	6.596	1.00	0.00
ATOM	1864	CA	SER	339	39.231	61.948	6.743	1.00	32.77
ATOM	1865	CB	SER	339	39.666	62.030	5.285	1.00	30.77
ATOM	1866	OG	SER	339	39.874	60.771	4.672	1.00	38.35
ATOM	1867	HG	SER	339	39.097	60.209	4.677	1.00	0.00
ATOM	1868	C	SER	339	38.181	63.015	6.948	1.00	32.35
ATOM	1869	O	SER	339	37.008	62.669	6.924	1.00	29.99
ATOM	1870	N	TRP	340	38.549	64.280	7.130	1.00	31.11
ATOM	1871	H	TRP	340	39.494	64.546	7.074	1.00	0.00
ATOM	1872	CA	TRP	340	37.580	65.306	7.447	1.00	32.42
ATOM	1873	CB	TRP	340	38.110	66.071	8.665	1.00	28.07
ATOM	1874	CG	TRP	340	38.069	65.153	9.851	1.00	31.22
ATOM	1875	CD2	TRP	340	36.790	64.901	10.522	1.00	33.69
ATOM	1876	CE2	TRP	340	37.281	63.820	11.450	1.00	38.45
ATOM	1877	CE3	TRP	340	35.473	65.302	10.526	1.00	37.14
ATOM	1878	CD1	TRP	340	39.112	64.394	10.320	1.00	32.03
ATOM	1879	NE1	TRP	340	38.611	63.616	11.256	1.00	35.26
ATOM	1880	HE1	TRP	340	39.143	62.912	11.687	1.00	0.00
ATOM	1881	CZ2	TRP	340	36.364	63.217	12.277	1.00	43.31
ATOM	1882	CZ3	TRP	340	34.612	64.660	11.389	1.00	42.02
ATOM	1883	CH2	TRP	340	35.043	63.639	12.227	1.00	45.40
ATOM	1884	C	TRP	340	37.260	66.265	6.311	1.00	35.22
ATOM	1885	O	TRP	340	38.137	66.652	5.544	1.00	36.37
ATOM	1886	N	ARG	341	35.989	66.670	6.210	1.00	37.03
ATOM	1887	H	ARG	341	35.321	66.289	6.821	1.00	0.00
ATOM	1888	CA	ARG	341	35.487	67.607	5.211	1.00	36.96
ATOM	1889	CB	ARG	341	34.687	66.815	4.170	1.00	34.84
ATOM	1890	CG	ARG	341	34.391	67.533	2.861	1.00	37.33
ATOM	1891	CD	ARG	341	33.517	66.655	1.972	1.00	39.02
ATOM	1892	NE	ARG	341	32.151	66.768	2.441	1.00	48.98
ATOM	1893	HE	ARG	341	31.684	67.621	2.324	1.00	0.00
ATOM	1894	CZ	ARG	341	31.501	65.767	3.031	1.00	51.01
ATOM	1895	NH1	ARG	341	32.089	64.556	3.232	1.00	56.13
ATOM	1896	HH11	ARG	341	33.030	64.400	2.934	1.00	0.00
ATOM	1897	HH12	ARG	341	31.577	63.821	3.676	1.00	0.00
ATOM	1898	NH2	ARG	341	30.219	65.962	3.440	1.00	58.28
ATOM	1899	HH21	ARG	341	29.777	66.848	3.294	1.00	0.00
ATOM	1900	HH22	ARG	341	29.720	65.218	3.884	1.00	0.00
ATOM	1901	C	ARG	341	34.616	68.684	5.864	1.00	37.23
ATOM	1902	O	ARG	341	33.969	68.486	6.883	1.00	38.61
ATOM	1903	N	HIS	342	34.550	69.880	5.324	1.00	39.36
ATOM	1904	H	HIS	342	35.002	70.055	4.471	1.00	0.00
ATOM	1905	CA	HIS	342	33.820	70.966	5.934	1.00	43.08
ATOM	1906	CB	HIS	342	34.885	71.921	6.463	1.00	41.90
ATOM	1907	CG	HIS	342	34.284	73.095	7.199	1.00	45.95
ATOM	1908	CD2	HIS	342	33.508	74.035	6.600	1.00	46.70
ATOM	1909	ND1	HIS	342	34.247	73.368	8.511	1.00	48.38
ATOM	1910	HD1	HIS	342	34.661	72.884	9.248	1.00	0.00
ATOM	1911	CE1	HIS	342	33.458	74.387	8.703	1.00	48.44

ATOM	1912	NE2	HIS	342	33.020	74.776	7.542	1.00	49.68
ATOM	1913	HE2	HIS	342	32.497	75.591	7.407	1.00	0.00
ATOM	1914	C	HIS	342	32.894	71.612	4.899	1.00	46.18
ATOM	1915	O	HIS	342	33.367	71.960	3.826	1.00	43.57
ATOM	1916	N	PRO	343	31.637	71.844	5.101	1.00	48.28
ATOM	1917	CD	PRO	343	30.984	71.752	6.398	1.00	46.23
ATOM	1918	CA	PRO	343	30.678	72.297	4.073	1.00	49.91
ATOM	1919	CB	PRO	343	29.387	72.590	4.824	1.00	44.40
ATOM	1920	CG	PRO	343	29.512	71.689	6.015	1.00	41.79
ATOM	1921	C	PRO	343	31.068	73.489	3.199	1.00	53.27
ATOM	1922	O	PRO	343	30.905	73.585	1.988	1.00	55.64
ATOM	1923	N	THR	344	31.615	74.459	3.909	1.00	54.13
ATOM	1924	H	THR	344	31.830	74.264	4.837	1.00	0.00
ATOM	1925	CA	THR	344	31.911	75.771	3.354	1.00	53.54
ATOM	1926	CB	THR	344	31.577	76.802	4.429	1.00	56.09
ATOM	1927	OG1	THR	344	31.901	76.175	5.672	1.00	63.15
ATOM	1928	HG1	THR	344	31.164	75.566	5.752	1.00	0.00
ATOM	1929	CG2	THR	344	30.088	77.164	4.490	1.00	57.44
ATOM	1930	C	THR	344	33.367	75.826	2.944	1.00	53.06
ATOM	1931	O	THR	344	33.802	76.516	2.046	1.00	53.90
ATOM	1932	N	MET	345	34.192	75.055	3.632	1.00	51.25
ATOM	1933	H	MET	345	33.844	74.348	4.202	1.00	0.00
ATOM	1934	CA	MET	345	35.604	75.172	3.363	1.00	52.69
ATOM	1935	CB	MET	345	36.357	75.229	4.662	1.00	60.31
ATOM	1936	CG	MET	345	36.128	76.474	5.498	1.00	71.30
ATOM	1937	SD	MET	345	36.752	76.178	7.176	1.00	86.57
ATOM	1938	CE	MET	345	38.405	76.807	7.073	1.00	81.62
ATOM	1939	C	MET	345	36.133	74.006	2.553	1.00	47.27
ATOM	1940	O	MET	345	37.288	74.042	2.179	1.00	48.63
ATOM	1941	N	GLY	346	35.383	72.947	2.236	1.00	40.77
ATOM	1942	H	GLY	346	34.439	72.892	2.503	1.00	0.00
ATOM	1943	CA	GLY	346	35.981	71.822	1.544	1.00	36.57
ATOM	1944	C	GLY	346	36.764	70.915	2.495	1.00	35.51
ATOM	1945	O	GLY	346	36.680	70.988	3.718	1.00	40.26
ATOM	1946	N	SER	347	37.567	70.012	1.949	1.00	32.41
ATOM	1947	H	SER	347	37.693	70.023	0.980	1.00	0.00
ATOM	1948	CA	SER	347	38.274	68.999	2.698	1.00	28.45
ATOM	1949	CB	SER	347	38.454	67.768	1.820	1.00	24.81
ATOM	1950	OG	SER	347	37.262	67.491	1.098	1.00	30.64
ATOM	1951	HG	SER	347	36.547	67.238	1.697	1.00	0.00
ATOM	1952	C	SER	347	39.631	69.491	3.157	1.00	31.86
ATOM	1953	O	SER	347	40.397	70.136	2.438	1.00	33.18
ATOM	1954	N	VAL	348	39.920	69.144	4.411	1.00	29.14
ATOM	1955	H	VAL	348	39.306	68.543	4.887	1.00	0.00
ATOM	1956	CA	VAL	348	41.127	69.588	5.086	1.00	25.67
ATOM	1957	CB	VAL	348	41.215	68.976	6.494	1.00	27.65
ATOM	1958	CG1	VAL	348	42.237	69.746	7.309	1.00	29.29
ATOM	1959	CG2	VAL	348	39.895	69.060	7.219	1.00	29.60
ATOM	1960	C	VAL	348	42.345	69.177	4.305	1.00	25.79
ATOM	1961	O	VAL	348	43.247	69.968	4.071	1.00	31.26
ATOM	1962	N	PHE	349	42.425	67.917	3.862	1.00	23.67
ATOM	1963	H	PHE	349	41.695	67.278	4.013	1.00	0.00
ATOM	1964	CA	PHE	349	43.621	67.455	3.181	1.00	22.69
ATOM	1965	CB	PHE	349	43.443	65.960	2.908	1.00	18.76
ATOM	1966	CG	PHE	349	44.459	65.361	1.941	1.00	20.55
ATOM	1967	CD1	PHE	349	44.029	64.916	0.702	1.00	14.77
ATOM	1968	CD2	PHE	349	45.790	65.223	2.311	1.00	15.53
ATOM	1969	CE1	PHE	349	44.918	64.278	-0.127	1.00	16.44
ATOM	1970	CE2	PHE	349	46.677	64.590	1.459	1.00	13.87
ATOM	1971	CZ	PHE	349	46.232	64.101	0.252	1.00	12.07
ATOM	1972	C	PHE	349	43.848	68.243	1.898	1.00	23.64
ATOM	1973	O	PHE	349	44.966	68.632	1.609	1.00	23.92
ATOM	1974	N	ILE	350	42.799	68.499	1.097	1.00	23.51
ATOM	1975	H	ILE	350	41.912	68.220	1.396	1.00	0.00

ATOM	1976	CA	ILE	350	42.969	69.170	-0.185	1.00	23.11
ATOM	1977	CB	ILE	350	41.617	69.131	-0.939	1.00	23.98
ATOM	1978	CG2	ILE	350	41.741	69.922	-2.229	1.00	24.02
ATOM	1979	CG1	ILE	350	41.200	67.689	-1.267	1.00	20.37
ATOM	1980	CD1	ILE	350	42.089	66.972	-2.272	1.00	14.33
ATOM	1981	C	ILE	350	43.451	70.600	0.073	1.00	23.87
ATOM	1982	O	ILE	350	44.428	71.058	-0.510	1.00	25.61
ATOM	1983	N	GLY	351	42.813	71.359	0.962	1.00	21.19
ATOM	1984	H	GLY	351	42.057	70.988	1.467	1.00	0.00
ATOM	1985	CA	GLY	351	43.248	72.720	1.212	1.00	19.54
ATOM	1986	C	GLY	351	44.702	72.800	1.640	1.00	26.25
ATOM	1987	O	GLY	351	45.524	73.568	1.138	1.00	28.41
ATOM	1988	N	ARG	352	45.064	71.963	2.614	1.00	28.53
ATOM	1989	H	ARG	352	44.388	71.391	3.045	1.00	0.00
ATOM	1990	CA	ARG	352	46.449	71.872	3.042	1.00	26.92
ATOM	1991	CB	ARG	352	46.589	70.842	4.167	1.00	31.79
ATOM	1992	CG	ARG	352	47.697	71.286	5.104	1.00	35.13
ATOM	1993	CD	ARG	352	47.091	71.997	6.310	1.00	38.95
ATOM	1994	NE	ARG	352	47.179	71.107	7.452	1.00	44.61
ATOM	1995	HE	ARG	352	47.920	70.468	7.491	1.00	0.00
ATOM	1996	CZ	ARG	352	46.307	71.116	8.449	1.00	41.51
ATOM	1997	NH1	ARG	352	46.502	70.272	9.494	1.00	48.56
ATOM	1998	HH11	ARG	352	47.294	69.660	9.507	1.00	0.00
ATOM	1999	HH12	ARG	352	45.849	70.267	10.251	1.00	0.00
ATOM	2000	NH2	ARG	352	45.227	71.943	8.435	1.00	44.65
ATOM	2001	HH21	ARG	352	45.080	72.554	7.657	1.00	0.00
ATOM	2002	HH22	ARG	352	44.570	71.936	9.187	1.00	0.00
ATOM	2003	C	ARG	352	47.419	71.483	1.931	1.00	26.87
ATOM	2004	O	ARG	352	48.535	71.995	1.866	1.00	26.27
ATOM	2005	N	LEU	353	47.033	70.567	1.037	1.00	25.01
ATOM	2006	H	LEU	353	46.156	70.135	1.143	1.00	0.00
ATOM	2007	CA	LEU	353	47.866	70.154	-0.070	1.00	23.26
ATOM	2008	CB	LEU	353	47.222	68.947	-0.778	1.00	25.55
ATOM	2009	CG	LEU	353	47.975	68.452	-2.020	1.00	23.59
ATOM	2010	CD1	LEU	353	49.420	68.121	-1.696	1.00	25.86
ATOM	2011	CD2	LEU	353	47.258	67.230	-2.552	1.00	29.54
ATOM	2012	C	LEU	353	48.034	71.303	-1.031	1.00	27.31
ATOM	2013	O	LEU	353	49.142	71.600	-1.485	1.00	24.83
ATOM	2014	N	ILE	354	46.923	71.977	-1.350	1.00	22.68
ATOM	2015	H	ILE	354	46.049	71.660	-1.035	1.00	0.00
ATOM	2016	CA	ILE	354	47.019	73.174	-2.168	1.00	24.25
ATOM	2017	CB	ILE	354	45.595	73.782	-2.327	1.00	21.11
ATOM	2018	CG2	ILE	354	45.652	75.176	-2.940	1.00	21.96
ATOM	2019	CG1	ILE	354	44.769	72.893	-3.248	1.00	17.07
ATOM	2020	CD1	ILE	354	43.279	73.267	-3.187	1.00	18.04
ATOM	2021	C	ILE	354	48.000	74.172	-1.540	1.00	25.12
ATOM	2022	O	ILE	354	48.967	74.616	-2.165	1.00	27.26
ATOM	2023	N	GLU	355	47.806	74.559	-0.276	1.00	27.20
ATOM	2024	H	GLU	355	47.040	74.212	0.235	1.00	0.00
ATOM	2025	CA	GLU	355	48.719	75.507	0.341	1.00	25.06
ATOM	2026	CB	GLU	355	48.501	75.685	1.803	1.00	32.73
ATOM	2027	CG	GLU	355	47.165	76.212	2.282	1.00	45.70
ATOM	2028	CD	GLU	355	47.053	75.777	3.746	1.00	58.26
ATOM	2029	OE1	GLU	355	45.921	75.683	4.245	1.00	61.90
ATOM	2030	OE2	GLU	355	48.092	75.513	4.385	1.00	61.89
ATOM	2031	C	GLU	355	50.150	75.114	0.242	1.00	23.42
ATOM	2032	O	GLU	355	51.029	75.893	-0.054	1.00	25.26
ATOM	2033	N	HIS	356	50.461	73.862	0.489	1.00	26.55
ATOM	2034	H	HIS	356	49.739	73.225	0.663	1.00	0.00
ATOM	2035	CA	HIS	356	51.855	73.438	0.432	1.00	26.58
ATOM	2036	CB	HIS	356	51.997	72.019	1.041	1.00	27.11
ATOM	2037	CG	HIS	356	51.846	72.065	2.551	1.00	23.74
ATOM	2038	CD2	HIS	356	52.890	72.264	3.421	1.00	22.80
ATOM	2039	ND1	HIS	356	50.728	72.044	3.288	1.00	25.98

ATOM	2040	HD1	HIS	356	49.819	71.907	2.953	1.00	0.00
ATOM	2041	CE1	HIS	356	51.036	72.231	4.550	1.00	19.00
ATOM	2042	NE2	HIS	356	52.333	72.360	4.608	1.00	22.63
ATOM	2043	HE2	HIS	356	52.814	72.450	5.460	1.00	0.00
ATOM	2044	C	HIS	356	52.411	73.447	-0.983	1.00	26.45
ATOM	2045	O	HIS	356	53.560	73.809	-1.239	1.00	20.78
ATOM	2046	N	MET	357	51.586	73.039	-1.948	1.00	17.38
ATOM	2047	H	MET	357	50.672	72.732	-1.747	1.00	0.00
ATOM	2048	CA	MET	357	52.037	73.060	-3.316	1.00	28.28
ATOM	2049	CB	MET	357	50.995	72.413	-4.239	1.00	30.75
ATOM	2050	CG	MET	357	50.860	70.870	-4.254	1.00	34.55
ATOM	2051	SD	MET	357	52.182	69.919	-5.054	1.00	43.28
ATOM	2052	CE	MET	357	51.449	69.433	-6.584	1.00	37.66
ATOM	2053	C	MET	357	52.249	74.503	-3.704	1.00	29.20
ATOM	2054	O	MET	357	53.237	74.846	-4.338	1.00	31.64
ATOM	2055	N	GLN	358	51.365	75.428	-3.360	1.00	25.95
ATOM	2056	H	GLN	358	50.539	75.168	-2.897	1.00	0.00
ATOM	2057	CA	GLN	358	51.650	76.808	-3.709	1.00	27.58
ATOM	2058	CB	GLN	358	50.505	77.693	-3.214	1.00	24.97
ATOM	2059	CG	GLN	358	49.262	77.438	-4.067	1.00	26.18
ATOM	2060	CD	GLN	358	48.063	78.234	-3.596	1.00	28.54
ATOM	2061	OE1	GLN	358	47.170	78.570	-4.362	1.00	30.13
ATOM	2062	NE2	GLN	358	47.919	78.558	-2.329	1.00	31.54
ATOM	2063	HE21	GLN	358	48.611	78.285	-1.693	1.00	0.00
ATOM	2064	HE22	GLN	358	47.124	79.077	-2.095	1.00	0.00
ATOM	2065	C	GLN	358	52.982	77.344	-3.182	1.00	30.98
ATOM	2066	O	GLN	358	53.783	77.971	-3.869	1.00	31.45
ATOM	2067	N	GLU	359	53.234	77.083	-1.906	1.00	32.65
ATOM	2068	H	GLU	359	52.581	76.563	-1.386	1.00	0.00
ATOM	2069	CA	GLU	359	54.425	77.558	-1.243	1.00	32.96
ATOM	2070	CB	GLU	359	54.178	77.382	0.251	1.00	37.33
ATOM	2071	CG	GLU	359	55.215	77.874	1.245	1.00	51.69
ATOM	2072	CD	GLU	359	55.241	79.379	1.308	1.00	63.61
ATOM	2073	OE1	GLU	359	54.197	79.992	1.550	1.00	70.65
ATOM	2074	OE2	GLU	359	56.320	79.940	1.132	1.00	69.55
ATOM	2075	C	GLU	359	55.638	76.809	-1.721	1.00	33.19
ATOM	2076	O	GLU	359	56.664	77.422	-1.974	1.00	36.20
ATOM	2077	N	TYR	360	55.584	75.475	-1.867	1.00	33.15
ATOM	2078	H	TYR	360	54.723	75.002	-1.843	1.00	0.00
ATOM	2079	CA	TYR	360	56.814	74.710	-2.053	1.00	28.52
ATOM	2080	CB	TYR	360	56.902	73.528	-1.079	1.00	30.16
ATOM	2081	CG	TYR	360	56.910	74.022	0.333	1.00	28.83
ATOM	2082	CD1	TYR	360	55.765	73.873	1.087	1.00	30.92
ATOM	2083	CE1	TYR	360	55.711	74.433	2.342	1.00	33.76
ATOM	2084	CD2	TYR	360	58.022	74.677	0.824	1.00	30.38
ATOM	2085	CE2	TYR	360	57.974	75.239	2.080	1.00	32.36
ATOM	2086	CZ	TYR	360	56.813	75.114	2.823	1.00	35.09
ATOM	2087	OH	TYR	360	56.737	75.692	4.073	1.00	41.75
ATOM	2088	HH	TYR	360	55.852	75.603	4.430	1.00	0.00
ATOM	2089	C	TYR	360	57.148	74.120	-3.389	1.00	27.85
ATOM	2090	O	TYR	360	58.243	73.583	-3.525	1.00	27.93
ATOM	2091	N	ALA	361	56.288	74.169	-4.411	1.00	27.66
ATOM	2092	H	ALA	361	55.459	74.682	-4.320	1.00	0.00
ATOM	2093	CA	ALA	361	56.544	73.494	-5.678	1.00	28.82
ATOM	2094	CB	ALA	361	55.328	73.717	-6.600	1.00	26.34
ATOM	2095	C	ALA	361	57.818	73.954	-6.355	1.00	32.26
ATOM	2096	O	ALA	361	58.461	73.249	-7.116	1.00	35.01
ATOM	2097	N	CYS	362	58.273	75.178	-6.133	1.00	38.50
ATOM	2098	H	CYS	362	57.694	75.795	-5.620	1.00	0.00
ATOM	2099	CA	CYS	362	59.576	75.578	-6.659	1.00	42.41
ATOM	2100	C	CYS	362	60.768	74.919	-5.987	1.00	41.51
ATOM	2101	O	CYS	362	61.761	74.529	-6.575	1.00	41.46
ATOM	2102	CB	CYS	362	59.746	77.086	-6.546	1.00	47.61
ATOM	2103	SG	CYS	362	61.400	77.655	-7.050	1.00	64.18

ATOM	2104	N	SER	363	60.741	74.757	-4.681	1.00	40.95
ATOM	2105	H	SER	363	59.909	74.803	-4.165	1.00	0.00
ATOM	2106	CA	SER	363	61.955	74.338	-4.026	1.00	43.35
ATOM	2107	CB	SER	363	62.122	75.236	-2.800	1.00	44.65
ATOM	2108	OG	SER	363	60.899	75.837	-2.362	1.00	53.93
ATOM	2109	HG	SER	363	60.553	76.414	-3.046	1.00	0.00
ATOM	2110	C	SER	363	61.985	72.866	-3.661	1.00	40.77
ATOM	2111	O	SER	363	63.036	72.255	-3.593	1.00	43.37
ATOM	2112	N	CYS	364	60.857	72.220	-3.399	1.00	38.31
ATOM	2113	H	CYS	364	59.976	72.633	-3.542	1.00	0.00
ATOM	2114	CA	CYS	364	60.937	70.839	-2.979	1.00	33.39
ATOM	2115	CB	CYS	364	60.056	70.623	-1.755	1.00	32.55
ATOM	2116	SG	CYS	364	60.508	71.767	-0.422	1.00	40.02
ATOM	2117	C	CYS	364	60.478	69.967	-4.121	1.00	29.84
ATOM	2118	O	CYS	364	59.610	70.346	-4.887	1.00	30.07
ATOM	2119	N	ASP	365	61.025	68.770	-4.300	1.00	28.01
ATOM	2120	H	ASP	365	61.859	68.579	-3.828	1.00	0.00
ATOM	2121	CA	ASP	365	60.406	67.784	-5.164	1.00	27.07
ATOM	2122	CB	ASP	365	61.379	66.619	-5.419	1.00	27.73
ATOM	2123	CG	ASP	365	61.757	65.825	-4.171	1.00	31.83
ATOM	2124	OD1	ASP	365	61.026	64.918	-3.783	1.00	34.71
ATOM	2125	OD2	ASP	365	62.805	66.094	-3.599	1.00	42.02
ATOM	2126	C	ASP	365	59.111	67.254	-4.538	1.00	28.95
ATOM	2127	O	ASP	365	58.838	67.420	-3.343	1.00	27.98
ATOM	2128	N	VAL	366	58.277	66.590	-5.336	1.00	27.55
ATOM	2129	H	VAL	366	58.544	66.434	-6.268	1.00	0.00
ATOM	2130	CA	VAL	366	56.968	66.183	-4.857	1.00	27.84
ATOM	2131	CB	VAL	366	56.251	65.513	-6.051	1.00	24.13
ATOM	2132	CG1	VAL	366	55.102	64.601	-5.672	1.00	23.78
ATOM	2133	CG2	VAL	366	55.629	66.654	-6.848	1.00	23.21
ATOM	2134	C	VAL	366	57.007	65.309	-3.611	1.00	28.22
ATOM	2135	O	VAL	366	56.256	65.536	-2.674	1.00	30.81
ATOM	2136	N	GLU	367	57.856	64.298	-3.489	1.00	28.49
ATOM	2137	H	GLU	367	58.450	64.111	-4.237	1.00	0.00
ATOM	2138	CA	GLU	367	57.867	63.516	-2.259	1.00	27.85
ATOM	2139	CB	GLU	367	58.939	62.428	-2.289	1.00	26.64
ATOM	2140	CG	GLU	367	58.553	61.219	-3.144	1.00	28.69
ATOM	2141	CD	GLU	367	59.442	60.019	-2.820	1.00	37.41
ATOM	2142	OE1	GLU	367	59.643	59.736	-1.632	1.00	42.87
ATOM	2143	OE2	GLU	367	59.937	59.388	-3.767	1.00	37.88
ATOM	2144	C	GLU	367	58.106	64.352	-1.012	1.00	28.61
ATOM	2145	O	GLU	367	57.604	64.052	0.059	1.00	31.13
ATOM	2146	N	GLU	368	58.872	65.437	-1.099	1.00	28.39
ATOM	2147	H	GLU	368	59.242	65.725	-1.959	1.00	0.00
ATOM	2148	CA	GLU	368	59.094	66.231	0.076	1.00	26.65
ATOM	2149	CB	GLU	368	60.278	67.145	-0.069	1.00	34.26
ATOM	2150	CG	GLU	368	61.017	66.888	1.244	1.00	53.59
ATOM	2151	CD	GLU	368	61.471	68.195	1.841	1.00	63.52
ATOM	2152	OE1	GLU	368	61.848	69.099	1.078	1.00	71.58
ATOM	2153	OE2	GLU	368	61.444	68.298	3.071	1.00	64.40
ATOM	2154	C	GLU	368	57.923	67.082	0.396	1.00	23.42
ATOM	2155	O	GLU	368	57.561	67.224	1.555	1.00	27.18
ATOM	2156	N	ILE	369	57.268	67.677	-0.591	1.00	22.22
ATOM	2157	H	ILE	369	57.595	67.596	-1.513	1.00	0.00
ATOM	2158	CA	ILE	369	56.027	68.395	-0.295	1.00	19.89
ATOM	2159	CB	ILE	369	55.403	68.931	-1.624	1.00	22.54
ATOM	2160	CG2	ILE	369	54.089	69.671	-1.355	1.00	20.28
ATOM	2161	CG1	ILE	369	56.360	69.917	-2.281	1.00	17.77
ATOM	2162	CD1	ILE	369	55.911	70.256	-3.701	1.00	15.38
ATOM	2163	C	ILE	369	55.024	67.497	0.435	1.00	20.18
ATOM	2164	O	ILE	369	54.331	67.885	1.371	1.00	20.19
ATOM	2165	N	PHE	370	54.923	66.241	0.020	1.00	21.39
ATOM	2166	H	PHE	370	55.470	65.932	-0.733	1.00	0.00
ATOM	2167	CA	PHE	370	53.962	65.359	0.654	1.00	23.30

ATOM	2168	CB	PHE	370	53.842	64.029	-0.121	1.00	23.30
ATOM	2169	CG	PHE	370	53.140	64.222	-1.451	1.00	23.92
ATOM	2170	CD1	PHE	370	53.037	63.153	-2.304	1.00	27.01
ATOM	2171	CD2	PHE	370	52.624	65.444	-1.841	1.00	29.88
ATOM	2172	CE1	PHE	370	52.427	63.311	-3.533	1.00	26.34
ATOM	2173	CE2	PHE	370	52.013	65.595	-3.069	1.00	27.67
ATOM	2174	CZ	PHE	370	51.906	64.521	-3.919	1.00	27.89
ATOM	2175	C	PHE	370	54.360	65.076	2.069	1.00	23.38
ATOM	2176	O	PHE	370	53.543	65.031	2.978	1.00	24.64
ATOM	2177	N	ARG	371	55.654	64.883	2.314	1.00	24.62
ATOM	2178	H	ARG	371	56.291	64.804	1.573	1.00	0.00
ATOM	2179	CA	ARG	371	56.103	64.783	3.683	1.00	26.21
ATOM	2180	CB	ARG	371	57.611	64.627	3.722	1.00	25.42
ATOM	2181	CG	ARG	371	57.954	64.338	5.180	1.00	26.24
ATOM	2182	CD	ARG	371	59.453	64.358	5.411	1.00	27.46
ATOM	2183	NE	ARG	371	60.022	65.650	5.122	1.00	34.21
ATOM	2184	HE	ARG	371	60.521	65.766	4.286	1.00	0.00
ATOM	2185	CZ	ARG	371	59.899	66.694	5.969	1.00	40.22
ATOM	2186	NH1	ARG	371	59.207	66.648	7.152	1.00	39.64
ATOM	2187	HH11	ARG	371	58.750	65.805	7.435	1.00	0.00
ATOM	2188	HH12	ARG	371	59.163	67.463	7.729	1.00	0.00
ATOM	2189	NH2	ARG	371	60.525	67.849	5.632	1.00	39.43
ATOM	2190	HH21	ARG	371	61.067	67.884	4.795	1.00	0.00
ATOM	2191	HH22	ARG	371	60.471	68.649	6.231	1.00	0.00
ATOM	2192	C	ARG	371	55.704	65.999	4.505	1.00	29.69
ATOM	2193	O	ARG	371	55.105	65.907	5.576	1.00	32.42
ATOM	2194	N	LYS	372	56.020	67.200	4.020	1.00	26.46
ATOM	2195	H	LYS	372	56.525	67.281	3.182	1.00	0.00
ATOM	2196	CA	LYS	372	55.576	68.377	4.733	1.00	23.67
ATOM	2197	CB	LYS	372	56.008	69.609	3.976	1.00	25.18
ATOM	2198	CG	LYS	372	57.506	69.718	4.053	1.00	21.18
ATOM	2199	CD	LYS	372	57.933	70.852	3.136	1.00	33.26
ATOM	2200	CE	LYS	372	59.042	71.666	3.789	1.00	42.84
ATOM	2201	NZ	LYS	372	58.499	72.323	4.969	1.00	50.90
ATOM	2202	HZ1	LYS	372	58.138	71.612	5.636	1.00	0.00
ATOM	2203	HZ2	LYS	372	57.717	72.944	4.674	1.00	0.00
ATOM	2204	HZ3	LYS	372	59.239	72.893	5.426	1.00	0.00
ATOM	2205	C	LYS	372	54.085	68.434	4.960	1.00	22.44
ATOM	2206	O	LYS	372	53.617	68.867	6.008	1.00	25.03
ATOM	2207	N	VAL	373	53.240	68.015	4.026	1.00	24.85
ATOM	2208	H	VAL	373	53.577	67.723	3.154	1.00	0.00
ATOM	2209	CA	VAL	373	51.813	67.977	4.333	1.00	26.14
ATOM	2210	CB	VAL	373	50.927	67.520	3.121	1.00	29.33
ATOM	2211	CG1	VAL	373	49.442	67.520	3.541	1.00	23.06
ATOM	2212	CG2	VAL	373	51.108	68.476	1.933	1.00	20.17
ATOM	2213	C	VAL	373	51.588	67.006	5.471	1.00	26.25
ATOM	2214	O	VAL	373	50.792	67.332	6.336	1.00	25.40
ATOM	2215	N	ARG	374	52.251	65.839	5.540	1.00	22.91
ATOM	2216	H	ARG	374	52.897	65.603	4.838	1.00	0.00
ATOM	2217	CA	ARG	374	52.025	64.926	6.660	1.00	24.92
ATOM	2218	CB	ARG	374	52.827	63.601	6.511	1.00	24.92
ATOM	2219	CG	ARG	374	52.332	62.777	5.307	1.00	26.50
ATOM	2220	CD	ARG	374	52.822	61.333	5.253	1.00	21.69
ATOM	2221	NE	ARG	374	54.262	61.249	5.278	1.00	21.59
ATOM	2222	HE	ARG	374	54.727	61.264	6.141	1.00	0.00
ATOM	2223	CZ	ARG	374	54.973	61.142	4.161	1.00	19.13
ATOM	2224	NH1	ARG	374	54.335	61.136	2.971	1.00	22.36
ATOM	2225	HH11	ARG	374	53.340	61.217	2.923	1.00	0.00
ATOM	2226	HH12	ARG	374	54.864	61.061	2.126	1.00	0.00
ATOM	2227	NH2	ARG	374	56.344	61.046	4.208	1.00	22.93
ATOM	2228	HH21	ARG	374	56.811	61.053	5.094	1.00	0.00
ATOM	2229	HH22	ARG	374	56.874	60.966	3.362	1.00	0.00
ATOM	2230	C	ARG	374	52.423	65.570	7.958	1.00	23.27
ATOM	2231	O	ARG	374	51.724	65.539	8.955	1.00	20.79

ATOM	2232	N	PHE	375	53.581	66.204	7.996	1.00	24.10
ATOM	2233	H	PHE	375	54.147	66.181	7.193	1.00	0.00
ATOM	2234	CA	PHE	375	54.025	66.896	9.187	1.00	23.34
ATOM	2235	CB	PHE	375	55.388	67.523	8.828	1.00	29.16
ATOM	2236	CG	PHE	375	56.010	68.272	9.989	1.00	35.30
ATOM	2237	CD1	PHE	375	56.926	67.655	10.803	1.00	36.99
ATOM	2238	CD2	PHE	375	55.684	69.589	10.221	1.00	33.65
ATOM	2239	CE1	PHE	375	57.518	68.348	11.838	1.00	36.47
ATOM	2240	CE2	PHE	375	56.281	70.277	11.255	1.00	38.44
ATOM	2241	CZ	PHE	375	57.202	69.659	12.064	1.00	37.61
ATOM	2242	C	PHE	375	52.982	67.917	9.664	1.00	28.21
ATOM	2243	O	PHE	375	52.775	68.135	10.857	1.00	28.91
ATOM	2244	N	SER	376	52.260	68.589	8.742	1.00	28.48
ATOM	2245	H	SER	376	52.414	68.468	7.783	1.00	0.00
ATOM	2246	CA	SER	376	51.281	69.562	9.208	1.00	28.11
ATOM	2247	CB	SER	376	50.715	70.398	8.047	1.00	24.30
ATOM	2248	OG	SER	376	49.984	69.740	7.034	1.00	26.36
ATOM	2249	HG	SER	376	50.480	68.972	6.709	1.00	0.00
ATOM	2250	C	SER	376	50.124	68.979	9.960	1.00	30.03
ATOM	2251	O	SER	376	49.395	69.683	10.647	1.00	27.69
ATOM	2252	N	PHE	377	49.927	67.671	9.838	1.00	33.33
ATOM	2253	H	PHE	377	50.511	67.127	9.265	1.00	0.00
ATOM	2254	CA	PHE	377	48.882	66.990	10.570	1.00	30.24
ATOM	2255	CB	PHE	377	48.276	65.883	9.691	1.00	21.45
ATOM	2256	CG	PHE	377	47.359	66.445	8.647	1.00	21.79
ATOM	2257	CD1	PHE	377	47.815	66.654	7.363	1.00	23.05
ATOM	2258	CD2	PHE	377	46.040	66.714	8.961	1.00	22.87
ATOM	2259	CE1	PHE	377	46.933	67.097	6.390	1.00	23.70
ATOM	2260	CE2	PHE	377	45.173	67.155	7.981	1.00	21.35
ATOM	2261	CZ	PHE	377	45.613	67.337	6.688	1.00	16.45
ATOM	2262	C	PHE	377	49.407	66.381	11.860	1.00	30.42
ATOM	2263	O	PHE	377	48.713	65.615	12.528	1.00	29.72
ATOM	2264	N	GLU	378	50.634	66.675	12.279	1.00	30.87
ATOM	2265	H	GLU	378	51.151	67.389	11.850	1.00	0.00
ATOM	2266	CA	GLU	378	51.169	65.910	13.374	1.00	35.50
ATOM	2267	CB	GLU	378	52.649	66.182	13.534	1.00	33.01
ATOM	2268	CG	GLU	378	53.146	64.886	14.168	1.00	38.65
ATOM	2269	CD	GLU	378	54.632	64.790	14.234	1.00	42.24
ATOM	2270	OE1	GLU	378	55.130	63.668	14.315	1.00	45.42
ATOM	2271	OE2	GLU	378	55.292	65.826	14.210	1.00	51.72
ATOM	2272	C	GLU	378	50.502	66.092	14.719	1.00	36.27
ATOM	2273	O	GLU	378	50.366	65.153	15.483	1.00	39.55
ATOM	2274	N	GLN	379	50.053	67.255	15.116	1.00	39.19
ATOM	2275	H	GLN	379	50.149	68.039	14.543	1.00	0.00
ATOM	2276	CA	GLN	379	49.268	67.367	16.328	1.00	48.22
ATOM	2277	CB	GLN	379	49.380	68.788	16.896	1.00	56.51
ATOM	2278	CG	GLN	379	50.771	69.437	16.941	1.00	63.32
ATOM	2279	CD	GLN	379	51.711	68.603	17.767	1.00	69.92
ATOM	2280	OE1	GLN	379	51.480	68.345	18.938	1.00	74.88
ATOM	2281	NE2	GLN	379	52.809	68.101	17.225	1.00	72.82
ATOM	2282	HE21	GLN	379	52.996	68.281	16.281	1.00	0.00
ATOM	2283	HE22	GLN	379	53.371	67.564	17.826	1.00	0.00
ATOM	2284	C	GLN	379	47.797	67.066	16.009	1.00	50.39
ATOM	2285	O	GLN	379	47.241	67.723	15.130	1.00	51.95
ATOM	2286	N	PRO	380	47.098	66.157	16.602	1.00	51.98
ATOM	2287	CD	PRO	380	47.634	65.095	17.439	1.00	50.16
ATOM	2288	CA	PRO	380	45.670	65.984	16.367	1.00	58.10
ATOM	2289	CB	PRO	380	45.261	64.815	17.243	1.00	53.72
ATOM	2290	CG	PRO	380	46.548	64.024	17.310	1.00	49.03
ATOM	2291	C	PRO	380	44.890	67.242	16.664	1.00	67.86
ATOM	2292	O	PRO	380	44.736	67.733	17.776	1.00	70.34
ATOM	2293	N	ASP	381	44.366	67.794	15.586	1.00	77.19
ATOM	2294	H	ASP	381	44.538	67.356	14.721	1.00	0.00
ATOM	2295	CA	ASP	381	43.596	69.021	15.617	1.00	83.19

ATOM	2296	CB	ASP	381	43.541	69.494	14.153	1.00	90.96
ATOM	2297	CG	ASP	381	43.014	70.910	13.938	1.00	908.27
ATOM	2298	OD1	ASP	381	43.143	71.746	14.843	1.00	11.43
ATOM	2299	OD2	ASP	381	42.481	71.167	12.846	1.00	102.13
ATOM	2300	C	ASP	381	42.223	68.750	16.235	1.00	83.61
ATOM	2301	O	ASP	381	41.197	69.227	15.766	1.00	86.07
ATOM	2302	N	GLY	382	42.096	67.981	17.316	1.00	80.88
ATOM	2303	H	GLY	382	42.906	67.764	17.831	1.00	0.00
ATOM	2304	CA	GLY	382	40.780	67.478	17.697	1.00	78.25
ATOM	2305	C	GLY	382	40.321	66.448	16.669	1.00	75.15
ATOM	2306	O	GLY	382	40.458	65.247	16.841	1.00	79.53
ATOM	2307	N	ARG	383	39.759	66.873	15.545	1.00	69.56
ATOM	2308	H	ARG	383	39.519	67.824	15.480	1.00	0.00
ATOM	2309	CA	ARG	383	39.629	66.003	14.381	1.00	64.31
ATOM	2310	CB	ARG	383	39.071	66.738	13.173	1.00	67.34
ATOM	2311	CG	ARG	383	37.832	67.576	13.414	1.00	69.84
ATOM	2312	CD	ARG	383	36.696	66.741	13.993	1.00	75.22
ATOM	2313	NE	ARG	383	35.525	67.573	14.194	1.00	78.64
ATOM	2314	HE	ARG	383	35.556	68.516	13.929	1.00	0.00
ATOM	2315	CZ	ARG	383	34.408	67.087	14.732	1.00	79.29
ATOM	2316	NH1	ARG	383	33.341	67.925	14.847	1.00	80.15
ATOM	2317	HH11	ARG	383	33.413	68.873	14.534	1.00	0.00
ATOM	2318	HH12	ARG	383	32.487	67.594	15.250	1.00	0.00
ATOM	2319	NH2	ARG	383	34.322	65.793	15.173	1.00	76.12
ATOM	2320	HH21	ARG	383	35.108	65.180	15.101	1.00	0.00
ATOM	2321	HH22	ARG	383	33.469	65.461	15.576	1.00	0.00
ATOM	2322	C	ARG	383	41.041	65.557	14.005	1.00	59.27
ATOM	2323	O	ARG	383	41.896	66.385	13.710	1.00	63.51
ATOM	2324	N	ALA	384	41.392	64.279	13.985	1.00	51.06
ATOM	2325	H	ALA	384	40.809	63.578	14.357	1.00	0.00
ATOM	2326	CA	ALA	384	42.711	63.902	13.518	1.00	43.97
ATOM	2327	CB	ALA	384	43.392	63.101	14.618	1.00	39.32
ATOM	2328	C	ALA	384	42.614	63.088	12.237	1.00	41.10
ATOM	2329	O	ALA	384	41.666	62.329	12.029	1.00	42.25
ATOM	2330	N	GLN	385	43.604	63.245	11.349	1.00	30.93
ATOM	2331	H	GLN	385	44.264	63.968	11.422	1.00	0.00
ATOM	2332	CA	GLN	385	43.794	62.325	10.258	1.00	26.81
ATOM	2333	CB	GLN	385	42.964	62.733	9.034	1.00	23.54
ATOM	2334	CG	GLN	385	43.318	64.098	8.481	1.00	27.75
ATOM	2335	CD	GLN	385	42.355	64.422	7.399	1.00	29.52
ATOM	2336	OE1	GLN	385	41.375	65.120	7.586	1.00	30.67
ATOM	2337	NE2	GLN	385	42.598	63.875	6.223	1.00	29.71
ATOM	2338	HE21	GLN	385	43.370	63.272	6.110	1.00	0.00
ATOM	2339	HE22	GLN	385	42.007	64.105	5.478	1.00	0.00
ATOM	2340	C	GLN	385	45.276	62.394	9.937	1.00	26.43
ATOM	2341	O	GLN	385	45.955	63.312	10.363	1.00	26.69
ATOM	2342	N	MET	386	45.844	61.457	9.197	1.00	25.50
ATOM	2343	H	MET	386	45.253	60.770	8.827	1.00	0.00
ATOM	2344	CA	MET	386	47.281	61.417	8.921	1.00	25.53
ATOM	2345	CB	MET	386	47.980	60.448	9.881	1.00	22.77
ATOM	2346	CG	MET	386	49.459	60.203	9.609	1.00	22.60
ATOM	2347	SD	MET	386	50.369	61.710	9.227	1.00	24.47
ATOM	2348	CE	MET	386	50.297	62.580	10.768	1.00	22.26
ATOM	2349	C	MET	386	47.376	60.904	7.503	1.00	25.56
ATOM	2350	O	MET	386	47.187	59.706	7.306	1.00	24.42
ATOM	2351	N	PRO	387	47.623	61.710	6.539	1.00	24.46
ATOM	2352	CD	PRO	387	47.479	63.144	6.670	1.00	25.50
ATOM	2353	CA	PRO	387	47.706	61.309	5.134	1.00	22.74
ATOM	2354	CB	PRO	387	47.813	62.609	4.355	1.00	21.24
ATOM	2355	CG	PRO	387	48.153	63.635	5.396	1.00	25.14
ATOM	2356	C	PRO	387	48.825	60.365	4.853	1.00	24.30
ATOM	2357	O	PRO	387	49.849	60.377	5.523	1.00	23.73
ATOM	2358	N	THR	388	48.671	59.504	3.859	1.00	22.51
ATOM	2359	H	THR	388	47.904	59.580	3.255	1.00	0.00

ATOM	2360	CA	THR	388	49.646	58.448	3.685	1.00	23.26
ATOM	2361	CB	THR	388	49.037	57.083	4.100	1.00	26.15
ATOM	2362	OG1	THR	388	48.399	57.238	5.359	1.00	34.81
ATOM	2363	HG1	THR	388	49.021	57.669	5.956	1.00	0.00
ATOM	2364	CG2	THR	388	50.105	56.009	4.257	1.00	24.27
ATOM	2365	C	THR	388	50.062	58.416	2.233	1.00	19.72
ATOM	2366	O	THR	388	49.262	58.508	1.316	1.00	20.10
ATOM	2367	N	THR	389	51.357	58.279	2.016	1.00	20.14
ATOM	2368	H	THR	389	51.974	58.285	2.771	1.00	0.00
ATOM	2369	CA	THR	389	51.933	58.099	0.709	1.00	22.14
ATOM	2370	CB	THR	389	53.304	58.762	0.775	1.00	22.05
ATOM	2371	OG1	THR	389	53.043	60.143	0.521	1.00	32.86
ATOM	2372	HG1	THR	389	52.584	60.204	-0.321	1.00	0.00
ATOM	2373	CG2	THR	389	54.305	58.266	-0.223	1.00	26.26
ATOM	2374	C	THR	389	51.981	56.611	0.446	1.00	27.05
ATOM	2375	O	THR	389	52.421	55.845	1.307	1.00	23.21
ATOM	2376	N	GLU	390	51.532	56.183	-0.742	1.00	23.67
ATOM	2377	H	GLU	390	51.265	56.821	-1.440	1.00	0.00
ATOM	2378	CA	GLU	390	51.461	54.770	-1.017	1.00	21.51
ATOM	2379	CB	GLU	390	49.993	54.334	-0.902	1.00	27.17
ATOM	2380	CG	GLU	390	49.716	54.258	0.612	1.00	35.02
ATOM	2381	CD	GLU	390	48.453	53.567	1.001	1.00	38.42
ATOM	2382	OE1	GLU	390	47.644	53.290	0.129	1.00	50.83
ATOM	2383	OE2	GLU	390	48.274	53.314	2.192	1.00	47.46
ATOM	2384	C	GLU	390	52.032	54.416	-2.351	1.00	22.05
ATOM	2385	O	GLU	390	52.148	55.236	-3.244	1.00	25.04
ATOM	2386	N	ARG	391	52.406	53.145	-2.449	1.00	20.72
ATOM	2387	H	ARG	391	52.314	52.613	-1.634	1.00	0.00
ATOM	2388	CA	ARG	391	52.871	52.472	-3.655	1.00	20.99
ATOM	2389	CB	ARG	391	51.677	52.087	-4.548	1.00	24.04
ATOM	2390	CG	ARG	391	51.351	50.594	-4.650	1.00	27.32
ATOM	2391	CD	ARG	391	51.041	50.062	-6.066	1.00	27.94
ATOM	2392	NE	ARG	391	49.890	49.159	-6.094	1.00	36.16
ATOM	2393	HE	ARG	391	49.248	49.211	-5.356	1.00	0.00
ATOM	2394	CZ	ARG	391	49.642	48.255	-7.068	1.00	38.21
ATOM	2395	NH1	ARG	391	50.302	48.156	-8.246	1.00	39.70
ATOM	2396	HH11	ARG	391	51.042	48.794	-8.455	1.00	0.00
ATOM	2397	HH12	ARG	391	50.046	47.453	-8.910	1.00	0.00
ATOM	2398	NH2	ARG	391	48.749	47.269	-6.849	1.00	47.46
ATOM	2399	HH21	ARG	391	48.279	47.209	-5.968	1.00	0.00
ATOM	2400	HH22	ARG	391	48.561	46.597	-7.567	1.00	0.00
ATOM	2401	C	ARG	391	53.842	53.303	-4.477	1.00	24.89
ATOM	2402	O	ARG	391	53.590	53.655	-5.630	1.00	24.46
ATOM	2403	N	VAL	392	54.998	53.634	-3.892	1.00	25.48
ATOM	2404	H	VAL	392	55.287	53.159	-3.085	1.00	0.00
ATOM	2405	CA	VAL	392	55.880	54.629	-4.494	1.00	21.84
ATOM	2406	CB	VAL	392	56.630	55.422	-3.404	1.00	19.22
ATOM	2407	CG1	VAL	392	57.408	56.628	-3.936	1.00	11.40
ATOM	2408	CG2	VAL	392	55.579	55.918	-2.436	1.00	18.72
ATOM	2409	C	VAL	392	56.865	53.948	-5.392	1.00	24.62
ATOM	2410	O	VAL	392	57.628	53.121	-4.915	1.00	20.00
ATOM	2411	N	THR	393	56.890	54.255	-6.691	1.00	23.61
ATOM	2412	H	THR	393	56.183	54.810	-7.081	1.00	0.00
ATOM	2413	CA	THR	393	57.958	53.731	-7.506	1.00	20.89
ATOM	2414	CB	THR	393	57.450	52.681	-8.535	1.00	21.30
ATOM	2415	OG1	THR	393	56.238	53.135	-9.148	1.00	22.68
ATOM	2416	HG1	THR	393	56.027	52.485	-9.822	1.00	0.00
ATOM	2417	CG2	THR	393	57.220	51.333	-7.855	1.00	17.80
ATOM	2418	C	THR	393	58.633	54.850	-8.235	1.00	22.52
ATOM	2419	O	THR	393	59.201	54.661	-9.303	1.00	22.98
ATOM	2420	N	LEU	394	58.605	56.072	-7.719	1.00	19.99
ATOM	2421	H	LEU	394	58.080	56.246	-6.913	1.00	0.00
ATOM	2422	CA	LEU	394	59.379	57.138	-8.338	1.00	20.68
ATOM	2423	CB	LEU	394	59.097	58.483	-7.647	1.00	18.77

ATOM	2424	CG	LEU	394	57.683	59.073	-7.778	1.00	17.38
ATOM	2425	CD1	LEU	394	57.642	60.395	-7.031	1.00	16.87
ATOM	2426	CD2	LEU	394	57.320	59.347	-9.243	1.00	17.98
ATOM	2427	C	LEU	394	60.851	56.789	-8.181	1.00	21.53
ATOM	2428	O	LEU	394	61.273	56.518	-7.073	1.00	21.60
ATOM	2429	N	THR	395	61.659	56.769	-9.243	1.00	24.17
ATOM	2430	H	THR	395	61.325	56.899	-10.160	1.00	0.00
ATOM	2431	CA	THR	395	63.090	56.503	-9.136	1.00	22.29
ATOM	2432	CB	THR	395	63.474	55.581	-10.303	1.00	19.28
ATOM	2433	OG1	THR	395	63.062	56.260	-11.471	1.00	22.57
ATOM	2434	HG1	THR	395	63.298	55.742	-12.244	1.00	0.00
ATOM	2435	CG2	THR	395	62.748	54.238	-10.343	1.00	15.70
ATOM	2436	C	THR	395	63.957	57.778	-9.146	1.00	23.98
ATOM	2437	O	THR	395	65.167	57.754	-8.943	1.00	25.97
ATOM	2438	N	ARG	396	63.362	58.947	-9.392	1.00	23.31
ATOM	2439	H	ARG	396	62.385	58.998	-9.428	1.00	0.00
ATOM	2440	CA	ARG	396	64.097	60.187	-9.519	1.00	26.02
ATOM	2441	CB	ARG	396	64.189	60.695	-10.936	1.00	28.35
ATOM	2442	CG	ARG	396	64.986	59.799	-11.825	1.00	32.64
ATOM	2443	CD	ARG	396	64.666	60.158	-13.248	1.00	43.18
ATOM	2444	NE	ARG	396	65.266	59.145	-14.075	1.00	51.29
ATOM	2445	HE	ARG	396	64.830	58.271	-14.157	1.00	0.00
ATOM	2446	CZ	ARG	396	66.403	59.385	-14.715	1.00	57.25
ATOM	2447	NH1	ARG	396	66.982	58.338	-15.382	1.00	62.75
ATOM	2448	HH11	ARG	396	66.539	57.441	-15.369	1.00	0.00
ATOM	2449	HH12	ARG	396	67.836	58.466	-15.885	1.00	0.00
ATOM	2450	NH2	ARG	396	66.961	60.635	-14.722	1.00	55.06
ATOM	2451	HH21	ARG	396	66.516	61.394	-14.247	1.00	0.00
ATOM	2452	HH22	ARG	396	67.815	60.786	-15.219	1.00	0.00
ATOM	2453	C	ARG	396	63.286	61.210	-8.805	1.00	25.66
ATOM	2454	O	ARG	396	62.133	60.990	-8.488	1.00	25.00
ATOM	2455	N	CYS	397	63.840	62.377	-8.546	1.00	27.52
ATOM	2456	H	CYS	397	64.766	62.545	-8.830	1.00	0.00
ATOM	2457	CA	CYS	397	63.114	63.404	-7.849	1.00	25.75
ATOM	2458	CB	CYS	397	64.086	64.447	-7.306	1.00	33.69
ATOM	2459	SG	CYS	397	65.267	63.936	-6.027	1.00	39.19
ATOM	2460	C	CYS	397	62.170	64.045	-8.834	1.00	24.55
ATOM	2461	O	CYS	397	62.531	64.263	-9.977	1.00	23.49
ATOM	2462	N	PHE	398	60.945	64.386	-8.464	1.00	21.44
ATOM	2463	H	PHE	398	60.638	64.172	-7.560	1.00	0.00
ATOM	2464	CA	PHE	398	60.072	65.094	-9.380	1.00	20.44
ATOM	2465	CB	PHE	398	58.677	64.374	-9.454	1.00	22.28
ATOM	2466	CG	PHE	398	57.644	65.009	-10.409	1.00	21.70
ATOM	2467	CD1	PHE	398	58.011	65.812	-11.494	1.00	26.69
ATOM	2468	CD2	PHE	398	56.306	64.770	-10.186	1.00	18.84
ATOM	2469	CE1	PHE	398	57.052	66.367	-12.329	1.00	27.09
ATOM	2470	CE2	PHE	398	55.358	65.320	-11.028	1.00	24.85
ATOM	2471	CZ	PHE	398	55.716	66.121	-12.095	1.00	25.47
ATOM	2472	C	PHE	398	59.960	66.512	-8.872	1.00	22.33
ATOM	2473	O	PHE	398	59.258	66.853	-7.926	1.00	22.03
ATOM	2474	N	TYR	399	60.703	67.377	-9.537	1.00	24.80
ATOM	2475	H	TYR	399	61.396	67.062	-10.144	1.00	0.00
ATOM	2476	CA	TYR	399	60.538	68.809	-9.395	1.00	25.89
ATOM	2477	CB	TYR	399	61.878	69.467	-9.624	1.00	25.90
ATOM	2478	CG	TYR	399	62.706	69.308	-8.397	1.00	27.28
ATOM	2479	CD1	TYR	399	63.584	68.255	-8.293	1.00	25.30
ATOM	2480	CE1	TYR	399	64.366	68.168	-7.155	1.00	33.32
ATOM	2481	CD2	TYR	399	62.601	70.258	-7.395	1.00	30.60
ATOM	2482	CE2	TYR	399	63.376	70.173	-6.258	1.00	31.42
ATOM	2483	CZ	TYR	399	64.262	69.125	-6.156	1.00	31.10
ATOM	2484	OH	TYR	399	65.009	68.999	-5.005	1.00	35.89
ATOM	2485	HH	TYR	399	65.683	68.322	-5.130	1.00	0.00
ATOM	2486	C	TYR	399	59.536	69.292	-10.432	1.00	27.64
ATOM	2487	O	TYR	399	59.668	69.103	-11.630	1.00	23.69

ATOM	2488	N	LEU	400	58.468	69.931	-10.000	1.00	24.40
ATOM	2489	H	LEU	400	58.337	70.072	-9.041	1.00	0.00
ATOM	2490	CA	LEU	400	57.598	70.629	-10.934	1.00	31.95
ATOM	2491	CB	LEU	400	56.310	71.032	-10.186	1.00	27.67
ATOM	2492	CG	LEU	400	55.445	69.821	-9.832	1.00	25.95
ATOM	2493	CD1	LEU	400	54.671	70.119	-8.568	1.00	26.52
ATOM	2494	CD2	LEU	400	54.550	69.476	-11.022	1.00	24.92
ATOM	2495	C	LEU	400	58.422	71.858	-11.293	1.00	36.21
ATOM	2496	O	LEU	400	59.402	72.088	-10.612	1.00	44.83
ATOM	2497	N	PHE	401	58.287	72.708	-12.295	1.00	36.07
ATOM	2498	H	PHE	401	57.660	72.565	-13.041	1.00	0.00
ATOM	2499	CA	PHE	401	59.210	73.839	-12.269	1.00	33.57
ATOM	2500	CB	PHE	401	60.245	73.706	-13.407	1.00	32.22
ATOM	2501	CG	PHE	401	61.399	72.857	-12.928	1.00	33.80
ATOM	2502	CD1	PHE	401	61.474	71.519	-13.260	1.00	32.31
ATOM	2503	CD2	PHE	401	62.416	73.423	-12.173	1.00	39.98
ATOM	2504	CE1	PHE	401	62.582	70.764	-12.892	1.00	33.77
ATOM	2505	CE2	PHE	401	63.512	72.653	-11.790	1.00	40.60
ATOM	2506	CZ	PHE	401	63.611	71.326	-12.167	1.00	36.46
ATOM	2507	C	PHE	401	58.367	75.031	-12.475	1.00	32.19
ATOM	2508	O	PHE	401	58.334	75.584	-13.558	1.00	29.45
ATOM	2509	N	PRO	402	57.638	75.512	-11.527	1.00	29.88
ATOM	2510	CD	PRO	402	57.751	75.159	-10.125	1.00	27.11
ATOM	2511	CA	PRO	402	56.710	76.609	-11.755	1.00	31.83
ATOM	2512	CB	PRO	402	56.137	76.946	-10.380	1.00	27.59
ATOM	2513	CG	PRO	402	57.161	76.376	-9.428	1.00	24.71
ATOM	2514	C	PRO	402	57.461	77.757	-12.427	1.00	37.62
ATOM	2515	O	PRO	402	58.588	78.123	-12.070	1.00	38.17
ATOM	2516	N	GLY	403	56.770	78.302	-13.431	1.00	37.83
ATOM	2517	H	GLY	403	55.816	78.096	-13.558	1.00	0.00
ATOM	2518	CA	GLY	403	57.339	79.300	-14.327	1.00	40.55
ATOM	2519	C	GLY	403	58.024	78.691	-15.553	1.00	39.74
ATOM	2520	O	GLY	403	58.363	79.436	-16.458	1.00	40.77
ATOM	2521	N	HIS	404	58.258	77.372	-15.646	1.00	40.90
ATOM	2522	H	HIS	404	57.856	76.702	-15.043	1.00	0.00
ATOM	2523	CA	HIS	404	59.038	76.818	-16.735	1.00	41.51
ATOM	2524	CB	HIS	404	60.391	76.313	-16.275	1.00	43.86
ATOM	2525	CG	HIS	404	61.057	77.377	-15.470	1.00	47.48
ATOM	2526	CD2	HIS	404	62.077	78.167	-15.913	1.00	46.94
ATOM	2527	ND1	HIS	404	60.694	77.798	-14.262	1.00	50.29
ATOM	2528	HD1	HIS	404	59.973	77.436	-13.710	1.00	0.00
ATOM	2529	CE1	HIS	404	61.438	78.828	-13.970	1.00	47.33
ATOM	2530	NE2	HIS	404	62.266	79.045	-14.963	1.00	49.11
ATOM	2531	HE2	HIS	404	62.923	79.771	-14.979	1.00	0.00
ATOM	2532	C	HIS	404	58.318	75.633	-17.302	1.00	41.65
ATOM	2533	O	HIS	404	58.804	75.085	-18.288	1.00	44.03
ATOM	2534	OT	HIS	404	57.304	75.238	-16.718	1.00	41.54
ATOM	2535	OH2	WAT	256	57.131	53.937	-16.157	1.00	21.86
ATOM	2536	H1	WAT	256	57.956	53.989	-16.611	1.00	0.00
ATOM	2537	H2	WAT	256	56.715	53.157	-16.559	1.00	0.00
ATOM	2538	OH2	WAT	257	59.288	45.222	-12.720	1.00	24.45
ATOM	2539	H1	WAT	257	59.678	44.463	-12.289	1.00	0.00
ATOM	2540	H2	WAT	257	59.326	45.020	-13.638	1.00	0.00
ATOM	2541	OH2	WAT	258	61.365	66.988	-12.454	1.00	18.38
ATOM	2542	H1	WAT	258	61.282	66.754	-11.566	1.00	0.00
ATOM	2543	H2	WAT	258	61.920	66.336	-12.878	1.00	0.00
ATOM	2544	OH2	WAT	259	54.401	52.311	-15.488	1.00	26.12
ATOM	2545	H1	WAT	259	53.455	52.320	-15.423	1.00	0.00
ATOM	2546	H2	WAT	259	54.685	52.959	-14.831	1.00	0.00
ATOM	2547	OH2	WAT	260	52.948	45.165	-10.748	1.00	22.53
ATOM	2548	H1	WAT	260	53.471	44.927	-9.991	1.00	0.00
ATOM	2549	H2	WAT	260	52.622	46.039	-10.552	1.00	0.00
ATOM	2550	OH2	WAT	261	39.932	72.422	-0.681	1.00	41.66
ATOM	2551	H1	WAT	261	40.131	72.039	0.168	1.00	0.00

ATOM	2552	H2	WAT	261	39.184	71.954	-1.011	1.00	0.00
ATOM	2553	OH2	WAT	262	40.595	65.620	4.462	1.00	27.37
ATOM	2554	H1	WAT	262	40.213	65.976	5.270	1.00	0.00
ATOM	2555	H2	WAT	262	39.866	65.614	3.842	1.00	0.00
ATOM	2556	OH2	WAT	263	59.703	63.723	-5.839	1.00	23.97
ATOM	2557	H1	WAT	263	59.734	63.118	-5.108	1.00	0.00
ATOM	2558	H2	WAT	263	59.203	63.239	-6.512	1.00	0.00
ATOM	2559	OH2	WAT	264	57.975	70.486	-7.257	1.00	26.26
ATOM	2560	H1	WAT	264	57.886	69.546	-7.232	1.00	0.00
ATOM	2561	H2	WAT	264	58.580	70.685	-6.537	1.00	0.00
ATOM	2562	OH2	WAT	265	49.889	74.051	7.407	1.00	51.01
ATOM	2563	H1	WAT	265	49.381	73.658	6.713	1.00	0.00
ATOM	2564	H2	WAT	265	49.717	74.986	7.331	1.00	0.00
ATOM	2565	OH2	WAT	266	55.224	73.467	-12.629	1.00	54.87
ATOM	2566	H1	WAT	266	56.050	73.568	-12.183	1.00	0.00
ATOM	2567	H2	WAT	266	55.324	73.889	-13.488	1.00	0.00
ATOM	2568	OH2	WAT	267	57.220	72.666	-15.238	1.00	33.22
ATOM	2569	H1	WAT	267	57.189	73.255	-16.021	1.00	0.00
ATOM	2570	H2	WAT	267	56.964	71.837	-15.606	1.00	0.00
ATOM	2571	OH2	WAT	268	35.858	66.670	-2.607	1.00	29.58
ATOM	2572	H1	WAT	268	36.152	66.629	-1.699	1.00	0.00
ATOM	2573	H2	WAT	268	35.860	67.587	-2.844	1.00	0.00
ATOM	2574	OH2	WAT	269	48.789	71.281	-21.710	1.00	49.48
ATOM	2575	H1	WAT	269	47.897	71.644	-21.837	1.00	0.00
ATOM	2576	H2	WAT	269	49.355	71.928	-22.109	1.00	0.00
ATOM	2577	OH2	WAT	270	59.440	63.444	-17.067	1.00	23.58
ATOM	2578	H1	WAT	270	59.959	62.711	-16.814	1.00	0.00
ATOM	2579	H2	WAT	270	58.513	63.193	-17.097	1.00	0.00
ATOM	2580	OH2	WAT	271	48.923	44.941	-15.001	1.00	59.67
ATOM	2581	H1	WAT	271	48.905	44.016	-14.762	1.00	0.00
ATOM	2582	H2	WAT	271	49.386	44.932	-15.826	1.00	0.00
ATOM	2583	OH2	WAT	272	44.435	59.093	9.639	1.00	24.08
ATOM	2584	H1	WAT	272	44.989	59.185	8.877	1.00	0.00
ATOM	2585	H2	WAT	272	44.990	58.678	10.300	1.00	0.00
ATOM	2586	OH2	WAT	273	53.920	52.043	-8.038	1.00	23.85
ATOM	2587	H1	WAT	273	54.603	52.710	-8.021	1.00	0.00
ATOM	2588	H2	WAT	273	54.232	51.362	-8.608	1.00	0.00
ATOM	2589	OH2	WAT	274	62.871	68.183	-1.698	1.00	38.92
ATOM	2590	H1	WAT	274	62.632	67.292	-1.909	1.00	0.00
ATOM	2591	H2	WAT	274	63.467	68.466	-2.393	1.00	0.00
ATOM	2592	OH2	WAT	275	46.942	70.044	-23.874	1.00	49.11
ATOM	2593	H1	WAT	275	47.058	69.784	-24.775	1.00	0.00
ATOM	2594	H2	WAT	275	47.406	69.414	-23.326	1.00	0.00
ATOM	2595	OH2	WAT	276	50.771	63.408	17.889	1.00	54.39
ATOM	2596	H1	WAT	276	50.872	64.350	17.946	1.00	0.00
ATOM	2597	H2	WAT	276	50.541	63.304	16.967	1.00	0.00
ATOM	2598	OH2	WAT	277	45.555	65.749	12.972	1.00	27.42
ATOM	2599	H1	WAT	277	46.291	65.423	12.436	1.00	0.00
ATOM	2600	H2	WAT	277	44.772	65.498	12.518	1.00	0.00
ATOM	2601	OH2	WAT	278	57.066	46.788	-11.771	1.00	27.22
ATOM	2602	H1	WAT	278	56.509	46.154	-12.204	1.00	0.00
ATOM	2603	H2	WAT	278	56.806	47.667	-12.005	1.00	0.00
ATOM	2604	OH2	WAT	279	50.499	65.012	-29.411	1.00	47.42
ATOM	2605	H1	WAT	279	50.711	64.860	-28.494	1.00	0.00
ATOM	2606	H2	WAT	279	51.009	65.791	-29.571	1.00	0.00
ATOM	2607	OH2	WAT	280	42.398	64.363	-27.639	1.00	73.43
ATOM	2608	H1	WAT	280	41.614	64.685	-28.072	1.00	0.00
ATOM	2609	H2	WAT	280	42.691	65.121	-27.145	1.00	0.00
ATOM	2610	OH2	WAT	281	47.580	50.658	-26.241	1.00	45.60
ATOM	2611	H1	WAT	281	47.146	51.280	-26.806	1.00	0.00
ATOM	2612	H2	WAT	281	48.027	50.065	-26.836	1.00	0.00
ATOM	2613	OH2	WAT	282	40.354	58.806	-25.242	1.00	51.46
ATOM	2614	H1	WAT	282	39.834	59.191	-25.936	1.00	0.00
ATOM	2615	H2	WAT	282	41.237	58.816	-25.588	1.00	0.00

ATOM	2616	OH2	WAT	283	59.582	57.507	-22.297	1.00	50.06
ATOM	2617	H1	WAT	283	59.205	58.060	-22.973	1.00	0.00
ATOM	2618	H2	WAT	283	60.461	57.302	-22.574	1.00	0.00
ATOM	2619	OH2	WAT	284	62.787	66.431	-21.929	1.00	64.67
ATOM	2620	H1	WAT	284	62.786	67.378	-21.776	1.00	0.00
ATOM	2621	H2	WAT	284	63.310	66.298	-22.709	1.00	0.00
ATOM	2622	OH2	WAT	285	42.178	68.676	-21.635	1.00	47.92
ATOM	2623	H1	WAT	285	42.226	68.152	-20.834	1.00	0.00
ATOM	2624	H2	WAT	285	41.528	68.220	-22.154	1.00	0.00
ATOM	2625	OH2	WAT	286	59.860	64.459	-20.626	1.00	45.90
ATOM	2626	H1	WAT	286	59.529	63.613	-20.882	1.00	0.00
ATOM	2627	H2	WAT	286	60.034	64.935	-21.429	1.00	0.00
ATOM	2628	OH2	WAT	287	38.592	60.429	-19.380	1.00	45.23
ATOM	2629	H1	WAT	287	37.765	59.995	-19.240	1.00	0.00
ATOM	2630	H2	WAT	287	38.339	61.266	-19.751	1.00	0.00
ATOM	2631	OH2	WAT	288	49.737	64.079	-19.712	1.00	31.09
ATOM	2632	H1	WAT	288	49.889	64.551	-20.540	1.00	0.00
ATOM	2633	H2	WAT	288	48.791	63.991	-19.646	1.00	0.00
ATOM	2634	OH2	WAT	289	45.077	74.284	-19.985	1.00	58.31
ATOM	2635	H1	WAT	289	44.803	75.186	-19.856	1.00	0.00
ATOM	2636	H2	WAT	289	45.225	73.984	-19.086	1.00	0.00
ATOM	2637	OH2	WAT	290	36.463	68.596	-18.372	1.00	41.38
ATOM	2638	H1	WAT	290	36.206	68.878	-19.244	1.00	0.00
ATOM	2639	H2	WAT	290	37.302	69.021	-18.240	1.00	0.00
ATOM	2640	OH2	WAT	291	42.509	73.175	-18.360	1.00	30.40
ATOM	2641	H1	WAT	291	42.018	73.868	-17.902	1.00	0.00
ATOM	2642	H2	WAT	291	41.926	72.928	-19.071	1.00	0.00
ATOM	2643	OH2	WAT	292	52.772	54.057	-17.864	1.00	34.00
ATOM	2644	H1	WAT	292	52.675	54.050	-16.919	1.00	0.00
ATOM	2645	H2	WAT	292	53.709	54.139	-17.997	1.00	0.00
ATOM	2646	OH2	WAT	293	58.499	51.544	-17.264	1.00	39.19
ATOM	2647	H1	WAT	293	58.896	50.712	-17.042	1.00	0.00
ATOM	2648	H2	WAT	293	59.231	52.121	-17.413	1.00	0.00
ATOM	2649	OH2	WAT	294	55.293	76.832	-15.365	1.00	77.96
ATOM	2650	H1	WAT	294	55.586	76.689	-14.489	1.00	0.00
ATOM	2651	H2	WAT	294	55.894	76.271	-15.896	1.00	0.00
ATOM	2652	OH2	WAT	295	50.254	47.990	-11.950	1.00	34.08
ATOM	2653	H1	WAT	295	49.709	48.063	-12.721	1.00	0.00
ATOM	2654	H2	WAT	295	49.755	47.316	-11.486	1.00	0.00
ATOM	2655	OH2	WAT	296	37.749	48.038	-8.897	1.00	50.16
ATOM	2656	H1	WAT	296	36.805	48.072	-8.734	1.00	0.00
ATOM	2657	H2	WAT	296	37.815	47.302	-9.501	1.00	0.00
ATOM	2658	OH2	WAT	297	61.144	72.978	-8.832	1.00	30.80
ATOM	2659	H1	WAT	297	62.021	72.636	-8.821	1.00	0.00
ATOM	2660	H2	WAT	297	61.120	73.515	-8.053	1.00	0.00
ATOM	2661	OH2	WAT	298	46.716	77.808	-7.102	1.00	36.58
ATOM	2662	H1	WAT	298	47.000	78.075	-6.217	1.00	0.00
ATOM	2663	H2	WAT	298	47.380	78.176	-7.649	1.00	0.00
ATOM	2664	OH2	WAT	299	43.918	76.808	-6.081	1.00	35.53
ATOM	2665	H1	WAT	299	43.850	77.750	-6.052	1.00	0.00
ATOM	2666	H2	WAT	299	44.809	76.650	-5.782	1.00	0.00
ATOM	2667	OH2	WAT	300	60.882	61.010	-5.837	1.00	32.21
ATOM	2668	H1	WAT	300	60.547	60.543	-5.092	1.00	0.00
ATOM	2669	H2	WAT	300	60.943	61.933	-5.683	1.00	0.00
ATOM	2670	OH2	WAT	301	56.234	77.147	-5.325	1.00	45.88
ATOM	2671	H1	WAT	301	55.449	77.454	-4.859	1.00	0.00
ATOM	2672	H2	WAT	301	56.348	77.843	-5.971	1.00	0.00
ATOM	2673	OH2	WAT	302	43.603	47.976	-4.116	1.00	46.63
ATOM	2674	H1	WAT	302	43.969	48.651	-4.654	1.00	0.00
ATOM	2675	H2	WAT	302	43.745	47.160	-4.601	1.00	0.00
ATOM	2676	OH2	WAT	303	41.712	55.660	-0.536	1.00	36.50
ATOM	2677	H1	WAT	303	41.333	54.851	-0.150	1.00	0.00
ATOM	2678	H2	WAT	303	42.325	55.359	-1.193	1.00	0.00
ATOM	2679	OH2	WAT	304	51.729	51.156	-0.590	1.00	72.02

ATOM	2680	H1	WAT	304	52.459	50.567	-0.423	1.00	0.00
ATOM	2681	H2	WAT	304	51.363	51.290	0.284	1.00	0.00
ATOM	2682	OH2	WAT	305	44.576	76.180	0.284	1.00	70.30
ATOM	2683	H1	WAT	305	44.696	75.258	0.070	1.00	0.00
ATOM	2684	H2	WAT	305	44.178	76.553	-0.493	1.00	0.00
ATOM	2685	OH2	WAT	306	38.913	54.669	0.203	1.00	39.19
ATOM	2686	H1	WAT	306	39.203	55.452	-0.255	1.00	0.00
ATOM	2687	H2	WAT	306	38.207	54.284	-0.306	1.00	0.00
ATOM	2688	OH2	WAT	307	42.134	58.338	1.150	1.00	29.79
ATOM	2689	H1	WAT	307	41.312	57.982	1.511	1.00	0.00
ATOM	2690	H2	WAT	307	42.564	57.551	0.838	1.00	0.00
ATOM	2691	OH2	WAT	308	56.648	60.941	0.737	1.00	38.97
ATOM	2692	H1	WAT	308	55.700	60.977	0.666	1.00	0.00
ATOM	2693	H2	WAT	308	56.928	61.839	0.383	1.00	0.00
ATOM	2694	OH2	WAT	309	45.030	48.554	9.192	1.00	48.96
ATOM	2695	H1	WAT	309	44.943	47.651	9.474	1.00	0.00
ATOM	2696	H2	WAT	309	45.909	48.606	8.834	1.00	0.00
ATOM	2697	OH2	WAT	310	41.590	59.650	10.888	1.00	32.65
ATOM	2698	H1	WAT	310	41.965	59.981	11.702	1.00	0.00
ATOM	2699	H2	WAT	310	41.171	60.430	10.534	1.00	0.00
ATOM	2700	OH2	WAT	311	30.678	62.812	10.599	1.00	48.30
ATOM	2701	H1	WAT	311	31.519	63.059	10.280	1.00	0.00
ATOM	2702	H2	WAT	311	30.787	61.904	10.876	1.00	0.00
ATOM	2703	OH2	WAT	312	44.035	51.425	12.296	1.00	49.62
ATOM	2704	H1	WAT	312	43.759	51.313	11.383	1.00	0.00
ATOM	2705	H2	WAT	312	43.889	50.557	12.653	1.00	0.00
ATOM	2706	OH2	WAT	313	53.084	69.483	13.408	1.00	45.11
ATOM	2707	H1	WAT	313	53.666	68.732	13.409	1.00	0.00
ATOM	2708	H2	WAT	313	52.885	69.526	12.474	1.00	0.00
ATOM	2709	OH2	WAT	314	33.280	54.578	14.147	1.00	71.20
ATOM	2710	H1	WAT	314	32.487	54.073	14.271	1.00	0.00
ATOM	2711	H2	WAT	314	33.372	54.689	13.208	1.00	0.00
ATOM	2712	OH2	WAT	315	60.509	60.787	-18.332	1.00	30.28
ATOM	2713	H1	WAT	315	60.849	61.538	-18.810	1.00	0.00
ATOM	2714	H2	WAT	315	60.079	61.112	-17.565	1.00	0.00
ATOM	2715	OH2	WAT	316	36.436	51.291	10.254	1.00	49.82
ATOM	2716	H1	WAT	316	36.114	50.786	9.515	1.00	0.00
ATOM	2717	H2	WAT	316	35.650	51.562	10.727	1.00	0.00
ATOM	2718	OH2	WAT	317	47.543	66.402	-29.189	1.00	49.95
ATOM	2719	H1	WAT	317	46.808	66.985	-29.300	1.00	0.00
ATOM	2720	H2	WAT	317	48.149	66.611	-29.900	1.00	0.00
ATOM	2721	OH2	WAT	318	39.908	61.653	-21.569	1.00	55.32
ATOM	2722	H1	WAT	318	39.811	62.356	-20.946	1.00	0.00
ATOM	2723	H2	WAT	318	40.435	61.009	-21.097	1.00	0.00
ATOM	2724	OH2	WAT	319	43.648	51.317	-20.053	1.00	55.22
ATOM	2725	H1	WAT	319	44.217	51.632	-19.345	1.00	0.00
ATOM	2726	H2	WAT	319	42.798	51.245	-19.643	1.00	0.00
ATOM	2727	OH2	WAT	320	42.904	66.185	-19.404	1.00	43.44
ATOM	2728	H1	WAT	320	43.844	66.182	-19.470	1.00	0.00
ATOM	2729	H2	WAT	320	42.797	66.244	-18.456	1.00	0.00
ATOM	2730	OH2	WAT	321	52.576	73.792	-19.312	1.00	47.88
ATOM	2731	H1	WAT	321	52.248	73.438	-18.497	1.00	0.00
ATOM	2732	H2	WAT	321	51.924	73.486	-19.932	1.00	0.00
ATOM	2733	OH2	WAT	322	61.556	50.185	-16.806	1.00	60.71
ATOM	2734	H1	WAT	322	60.747	49.697	-16.824	1.00	0.00
ATOM	2735	H2	WAT	322	62.307	49.596	-16.932	1.00	0.00
ATOM	2736	OH2	WAT	323	24.851	56.075	-3.153	1.00	38.05
ATOM	2737	H1	WAT	323	25.114	55.419	-2.507	1.00	0.00
ATOM	2738	H2	WAT	323	25.365	55.812	-3.916	1.00	0.00
ATOM	2739	OH2	WAT	324	30.036	71.409	-2.744	1.00	45.31
ATOM	2740	H1	WAT	324	29.383	70.770	-3.022	1.00	0.00
ATOM	2741	H2	WAT	324	29.785	71.599	-1.852	1.00	0.00
ATOM	2742	OH2	WAT	325	33.127	79.276	0.558	1.00	57.23
ATOM	2743	H1	WAT	325	33.528	79.402	-0.294	1.00	0.00

ATOM	2744	H2	WAT	325	32.600	80.047	0.708	1.00	0.00
ATOM	2745	OH2	WAT	326	35.907	47.459	2.721	1.00	52.14
ATOM	2746	H1	WAT	326	35.224	48.120	2.665	1.00	0.00
ATOM	2747	H2	WAT	326	36.753	47.864	2.620	1.00	0.00
ATOM	2748	OH2	WAT	327	54.215	72.016	6.546	1.00	52.02
ATOM	2749	H1	WAT	327	55.027	71.530	6.405	1.00	0.00
ATOM	2750	H2	WAT	327	54.516	72.859	6.883	1.00	0.00
ATOM	2751	OH2	WAT	328	41.269	52.487	1.122	1.00	51.87
ATOM	2752	H1	WAT	328	40.694	51.781	1.440	1.00	0.00
ATOM	2753	H2	WAT	328	42.127	52.127	1.259	1.00	0.00
ATOM	2754	OH2	WAT	329	34.066	58.806	13.164	1.00	55.71
ATOM	2755	H1	WAT	329	34.724	59.474	13.292	1.00	0.00
ATOM	2756	H2	WAT	329	34.564	58.010	12.945	1.00	0.00
ATOM	2757	OH2	WAT	330	41.816	52.756	13.918	1.00	44.03
ATOM	2758	H1	WAT	330	42.281	53.408	13.395	1.00	0.00
ATOM	2759	H2	WAT	330	42.525	52.335	14.395	1.00	0.00
ATOM	2760	OH2	WAT	331	39.370	62.098	14.302	1.00	54.70
ATOM	2761	H1	WAT	331	38.736	62.661	14.727	1.00	0.00
ATOM	2762	H2	WAT	331	39.761	62.569	13.574	1.00	0.00
ATOM	2763	OH2	WAT	332	50.309	69.365	13.364	1.00	54.23
ATOM	2764	H1	WAT	332	50.055	69.719	12.508	1.00	0.00
ATOM	2765	H2	WAT	332	51.043	69.910	13.645	1.00	0.00
ATOM	2766	OH2	WAT	333	40.562	55.451	15.773	1.00	61.39
ATOM	2767	H1	WAT	333	39.723	55.080	16.041	1.00	0.00
ATOM	2768	H2	WAT	333	40.748	55.017	14.937	1.00	0.00

The following abbreviations are used in Table B.

"Atom type" refers to the element whose coordinates are measured. The first letter in the column defines the element.

"X, Y, Z" crystallographically define the atomic position of the element measured.

"B" is a thermal factor that measures movement of the atom around its atomic center.

Atoms numbered 153-158 (Lys-146) and 184-189 (Ser-149) were modeled as Ala residues.

Atoms numbered 1487-1534 and designated "Ald" in the column titled "Residue" are Cys-285 bound to the tetrapeptide aldehyde inhibitor.

Structure coordinates for ICE according to Table B may be modified from this original set by mathematical manipulation. Such manipulations include, but are not limited to, crystallographic permutations of the raw structure coordinates, fractionalization of the raw structure coordinates, integer additions or subtractions to sets of the raw structure coordinates,

inversion of the raw structure coordinates, and any combination of the above.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
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(ii) TITLE OF INVENTION: CRYSTAL STRUCTURE AND MUTANTS OF INTERLEUKIN-1 BETA CONVERTING ENZYME

(iii) NUMBER OF SEQUENCES: 1

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/261,582
(B) FILING DATE: 17-JUN-1994

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser
1               5                   10                  15

Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr
            20                  25                  30
```

Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
35 40 45

Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
50 55 60

Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
65 70 75 80

Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly
85 90 95

Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val Leu Ser Ser Phe Pro
100 105 110

Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser Ser Gly
115 120 125

Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln Arg Ile
130 135 140

Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser
145 150 155 160

Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile
165 170 175

Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu
180 185 190

Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala
195 200 205

Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His
210 215 220

Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg
225 230 235 240

Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu
245 250 255

Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser
260 265 270

Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Cys Arg Gly Asp
275 280 285

Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn
290 295 300

Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile Lys Lys
305 310 315 320

```
Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp
                325                 330                 335

Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg
            340                 345                 350

Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser Cys Asp Val Glu Glu
        355                 360                 365

Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala
    370                 375                 380

Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr Arg Cys Phe Tyr Leu
385                 390                 395                 400

Phe Pro Gly His
```

CLAIMS

We claim:

1. An interleukin-1ß converting enzyme crystal, wherein said crystal has tetragonal space group symmetry $P4_32_12$.

2. The interleukin-1ß converting enzyme crystal according to claim 1, wherein said crystal comprises rectangular shaped unit cells, each unit cell having the dimensions a=b=65 ± 5Å, and c=162 ± 5Å.

3. The interleukin-1ß converting enzyme crystal according to claim 1, wherein said enzyme is a tetramer.

4. The interleukin-1ß converting enzyme crystal according to claim 3, wherein said tetramer comprises two adjacent p10 subunits contacted by two p20 subunits, said p10 subunits interacting across the two-fold axis of said crystal.

5. The interleukin-1ß converting enzyme crystal according to claim 4, wherein said enzyme is characterized by an active site moiety characterized by at least amino acids 173, 176, 177, 178, 179, 180, 236, 237, 238, 239, 244, 248, 283, 284, 285, 290, 338, 339, 340, 341, 342, 343, 344, 345, 348, 352, 381 and 383 of SEQ. ID NO:1.

6. The interleukin-1ß converting enzyme crystal according to claim 5, wherein said active site moiety comprises amino acids from said p10 and p20 subunits.

7. The interleukin-1ß converting enzyme crystal according to claim 4, wherein said enzyme is characterized by an accessory binding site moiety characterized by at least amino acids 150, 151, 240, 259, 267, 268, 274, 291, 292, 293, 294, 295, 296, 297, 317, 318, 319, 320, 321, 322, 323, 324, 325, 327, 334, 335, 367, 371, 374, 375, 377, 378, 380, 382, 384, 386, 388, 389, 390, 391, 392, 393, 394, 395 and 396 of SEQ. ID NO:1.

8. The interleukin-1ß converting enzyme crystal according to claim 7, wherein said accessory binding site moiety comprises amino acids adjacent to said two-fold axis according to Table A.

9. The interleukin-1ß converting enzyme crystal according to any one of claims 1 to 8, wherein said enzyme is characterized by structure coordinates according to Table B.

10. A heavy atom derivative of a crystal, said crystal being selected from the group consisting of crystals of ICE, crystals of ICE mutants, crystals of ICE homologues or crystals of co-complexes of ICE.

11. The heavy atom derivative according to claim 10, wherein said derivative is formed by the reaction of said crystal with a compound selected from the group consisting of thimerosal, gold thiomalate, uranyl acetate and lead chloride.

12. The use of the structure coordinates of interleukin-1ß converting enzyme, or portions thereof, to solve a crystal form of a mutant, homologue or co-complex of interleukin-1ß converting enzyme by molecular replacement.

13. The use of the structure coordinates of interleukin-1ß converting enzyme to computationally evaluate a chemical entity for associating with the active site or the accessory binding site of interleukin-1ß converting enzyme.

14. The use of the structure coordinates of interleukin-1ß converting enzyme to design a compound capable of associating with the active site or the accessory binding site of interleukin-1ß converting enzyme.

15. The use of the structure coordinates of interleukin-1ß converting enzyme according to claim 13 or 14, wherein a compound that is characterized by the chemical entity that associates with said active site or said accessory binding site, is an inhibitor of interleukin-1ß converting enzyme.

16. The use of the structure coordinates according to claim 15, wherein said inhibitor is a non-competitive or uncompetitive inhibitor of interleukin-1ß converting enzyme.

17. The use of the structure coordinates of interleukin-1ß converting enzyme to determine the orientation of ligands in the active site or in the accessory binding site of interleukin-1ß converting enzyme.

18. The use of the structure coordinates of interleukin-1ß converting enzyme to identify an intermediate in a chemical reaction between said enzyme and a compound which is an ICE substrate or an ICE inhibitor.

19. The use of the structure coordinates of interleukin-1ß converting enzyme according to any one of claims 12 to 14 or 17 to 18, wherein said structure coordinates are according to Table B.

20. The use of the structure coordinates of interleukin-1ß converting enzyme according to claim 15, wherein said structure coordinates are according to Table B.

21. The use of the structure coordinates of interleukin-1ß converting enzyme according to claim 16, wherein said structure coordinates are according to Table B.

22. An interleukin-1ß converting enzyme, wherein one or more of the amino acids in the active site or in the accessory binding site are replaced by one or more amino acids selected from the group consisting of naturally occurring amino acids, unnatural amino acids, selenocysteine and selenomethionine.

23. The interleukin-1ß converting enzyme according to claim 22, wherein a hydrophilic or hydrophobic amino acid residue in said active site or said accessory binding site is replaced.

24. The interleukin-1ß converting enzyme according to claim 22, wherein said active site amino acid is selected from the group consisting of amino acids 173, 176, 177, 178, 179, 180, 236, 237, 238, 239, 244, 248, 283, 284, 285, 290, 338, 339, 340, 341, 342, 343, 345, 348, 352, 381 and 383 of SEQ. ID NO:1.

25. The interleukin-1ß converting enzyme according to claim 22, wherein said accessory binding site amino acid is selected from the group consisting of amino acids 150, 151, 240, 259, 267, 268, 274, 291, 292, 293, 294, 295, 296, 297, 317, 318, 319, 320, 321, 322, 323, 324, 325, 327, 334, 335, 367, 371, 374, 375, 377, 378, 380, 382, 384, 386, 388, 389, 390, 391, 392, 393, 394, 395 and 396 of SEQ. ID NO:1.

26. The interleukin-1ß converting enzyme according to claim 22, wherein at least one cysteine amino acid is replaced by an amino acid selected from the group consisting of selenocysteine or selenomethionine.

27. The interleukin-1ß converting enzyme according to claim 22, wherein at least one methionine amino acid is replaced by an amino acid selected from the group consisting of selenocysteine or selenomethionine.

28. The interleukin-1ß converting enzyme according to any one of claims 22 to 27, wherein said enzyme is in crystalline form.

29. The interleukin-1ß converting enzyme according to claim 22, wherein said enzyme is characterized by increased stability to subunit dissociation.

30. The interleukin-1ß converting enzyme according to claim 22, said enzyme having higher specific activity than the wild-type enzyme.

31. The interleukin-1ß converting enzyme according to claim 22, said enzyme having altered substrate specificity.

32. The use of an interleukin-1ß converting enzyme according to claim 22 to determine binding interactions between a chemical compound and the enzyme.

33. An interleukin-1ß converting enzyme, wherein at least one amino acid residue on, at or near the surface of said enzyme is replaced, resulting in an altered surface charge of one or more charge units.

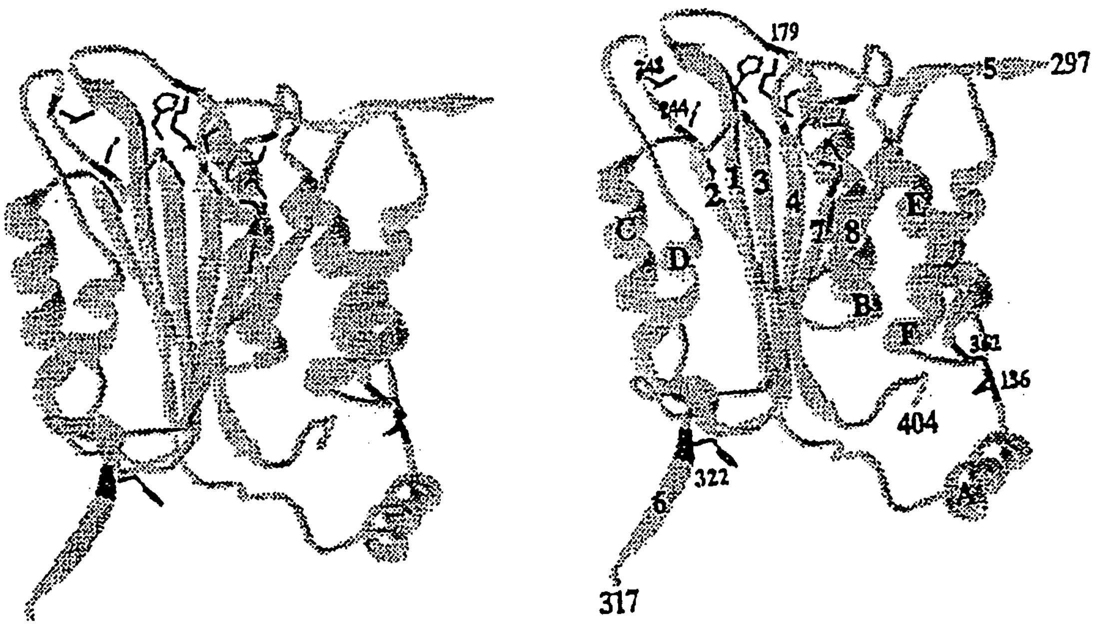


FIGURE 1

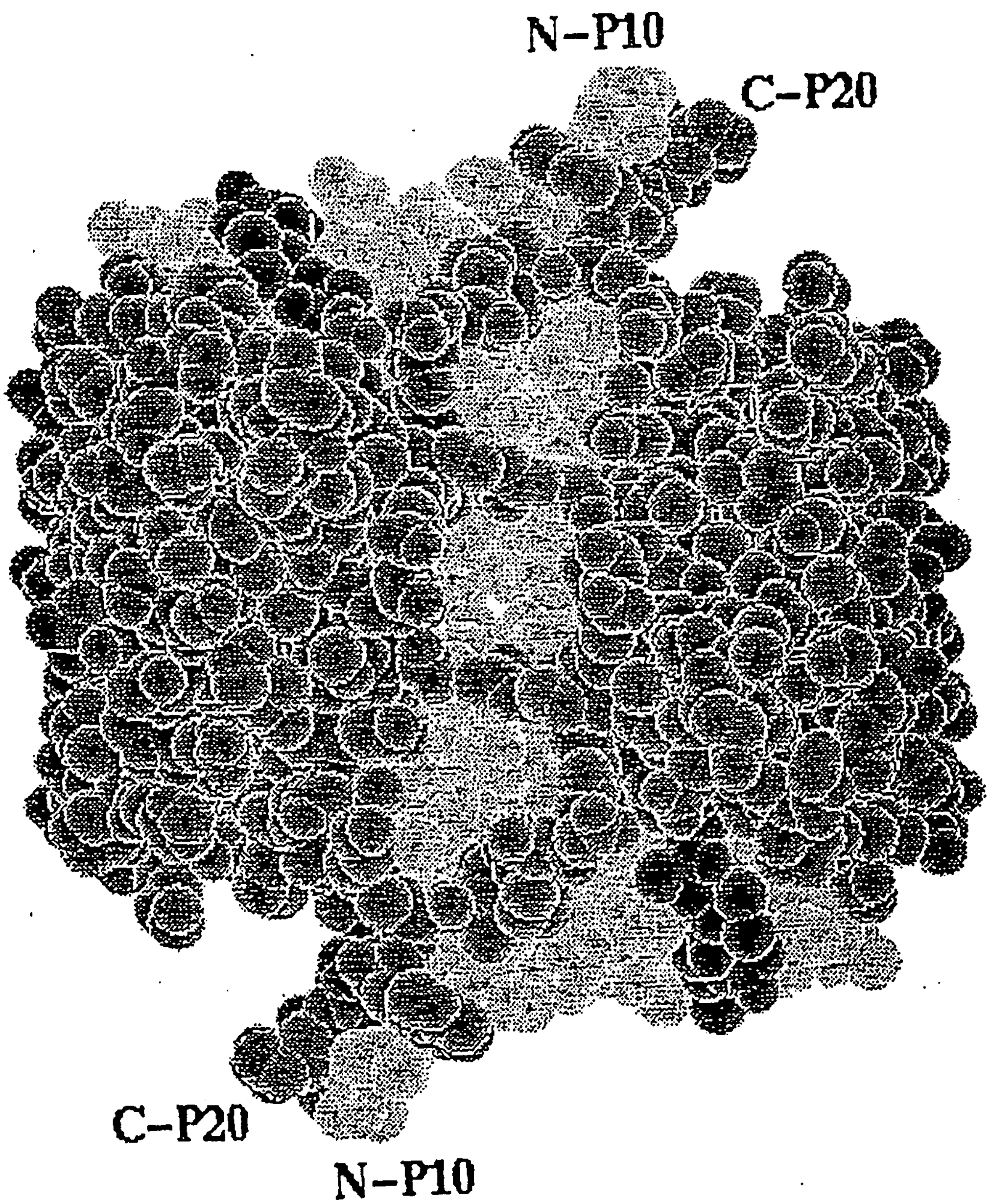
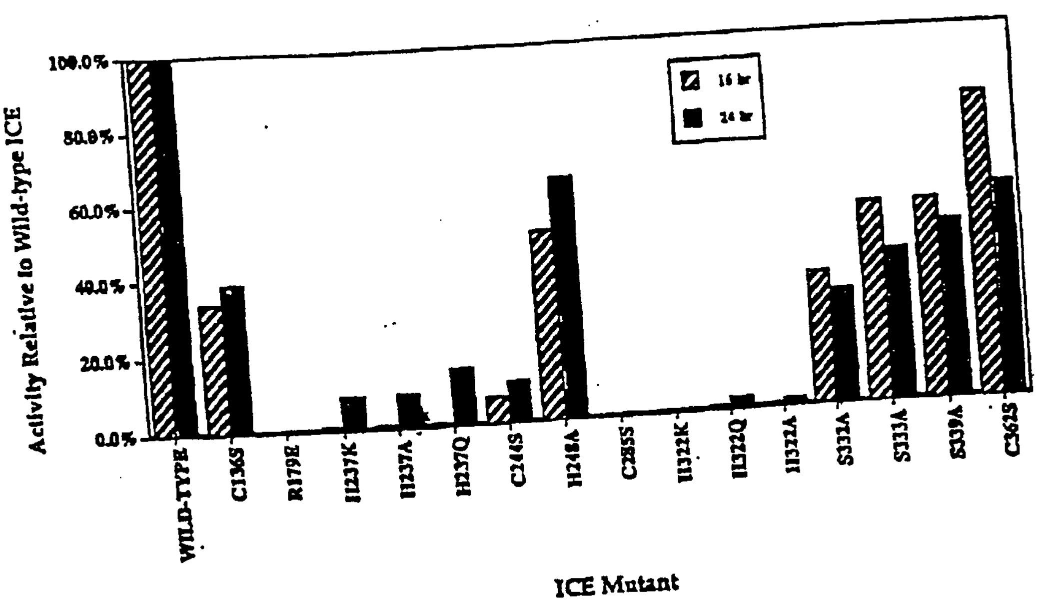


FIGURE 2



100.0%
80.0%
60.0%
40.0%
20.0%
0.0%
Activity Relative to Wild-type ICE
16 hr
24 hr
WILD-TYPE
C136S
R179E
H237K
H237A
H237Q
C244S
H248A
C285S
H322K
H322Q
H322A
S332A
S333A
S339A
C362S
ICE Mutant

FIGURE 3

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/07619

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N9/64 C12Q1/37 According to International Patent Classification (IPC) or to both national classification and IPC	
B. FIELDS SEARCHED	
Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12N	
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched	
Electronic data base consulted during the international search (name of data base and, where practical, search terms used)	

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X Y	JOURNAL OF CELLULAR BIOCHEMISTRY, SUPPLEMENT, vol. 18D, 5 - 12 March 1994 page 148 J. THOMSON ET AL 'In vito folding and autoprocessing of active interleukin-1 beta converting enzyme from an inactive recombinant precursor' see abstract S 229 ---	1-9 10-33
X Y	WO,A,94 00154 (MERCK & CO INC ;HOWARD ANDREW D (US); MOLINEAUX SUSAN M (US); TOCC) 6 January 1994 see the whole document --- -/--	1-9 10-33

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

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Date of the actual completion of the international search	Date of mailing of the international search report
23 October 1995	29.11.95
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Van der Schaal, C

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	NATURE, vol. 356, 30 April 1992 pages 768-774, N. THORNBERRY ET AL 'A novel heterodimeric cysteine protease is required for interleukin-1-beta processing in monocytes' cited in the application see page 771, right column, line 2 - page 773	22-25,28
A	BIOTECH. ADV, vol. 5, 1987 pages 221-234, P. BRYAN 'Protein engineering'	1-9
Y	see the whole document especially page 222, last two sentences	10-33
A	I. CAMPBELL AND R. DWEK 'Biological Spectroscopy' 1984 , THE BENJAMIN/CUMMINGS PUBLISHING COMPANY , MENLO PARK, USA	1-9
Y	see Chapter 12, especially page 299, last paragraph; page 320-328	10-33
A	PROTEIN ENGINEERING, vol. 6, no. 6, 1 August 1993 pages 615-620, XP 000385582 KAJIHARA A 'PROTEIN MODELLING USING A CHIMERA REFERENCE PROTEIN DERIVED FROM EXONS'	1-9
Y	see introduction	12-33
A	NATURE, vol. 328, 6 August 1987 pages 496-500, A. RUSSELL 'Rational modification of enzyme catalysis by engineering surface charge'	1-9
Y	see the whole document	12-33
A	NATURE, vol. 221, 1969 pages 235-242, C. SCHUBERT WRIGHT ET AL 'Structure of Subtilisin BPN' at 2.5A resolution' see the whole document	10-33

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INTERNATIONAL SEARCH REPORT

Intern al Application No
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	THE EMBO JOURNAL, vol. 10, no. 9, 1991 pages 2321-2330, D. MUSIL ET AL 'The refined 2.15A X-ray crystal structure of human liver cathepsin B: the structural basis for its specificity' see the whole document ---	12-33
A	SCIENCE, vol. 243, March 1989 pages 1346-1351, A. SIELECKI ET AL 'Structure of recombinant human renin, a target for cardiovascular-active drugs, at 2.5A resolution' see the whole document ---	12-33
P,X	NATURE (LONDON) (1994), 370(6487), 270-5 CODEN: NATUAS;ISSN: 0028-0836, 1994 WILSON, KEITH P. ET AL 'Structure and mechanism of interleukin -1.beta. converting enzyme' see the whole document ---	1-33
P,X	CELL (CAMBRIDGE, MASS.) (1994), 78(2), 343-52 CODEN: CELLB5;ISSN: 0092-8674, 1994 WALKER, N. P. C. ET AL 'Crystal structure of the cysteine protease interleukin -1.beta.- converting enzyme: a (p20/p10)2 homodimer' see the whole document -----	1-33

INTERNATIONAL SEARCH REPORT

Intern al Application No
PCT/US 95/07619

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WO-A-9400154	06-01-94	AU-B- 4634993	24-01-94
		CA-A- 2076159	17-02-93
		CA-A- 2136981	06-01-94
		EP-A- 0648128	19-04-95